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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

MasPar time 3.25 Seconds 39.202 Million cell updates/sec Thu Oct 28 11:19:27 1999; Run on:

Tabular output not generated

(1-6) from US09081707.pep 39 >US-09-081-707-7 Description: Perfect Score:

1 HSSKLQ 6 Sequence:

Scoring table:

170751 seqs, 21266608 residues PAM 150 Gap 15 Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

a-geneseq35 Database:

scale 0.446 Variance 29.123; Mean 12.999; Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Pred. No.	1.78e+02	1.78e+02	cida- 2.46e+02	chain 3.38e+02	A-enc 3.38e+02	cific 3.38e+02	chain 3.38e+02	chain 3.38e+02	able 3.38e+02	chain 3.38e+02	chain 3.38e+02	chain 3.38e+02	nscri 3.38e+02	e. 3.38e+02	chain 3.38e+02	antig 4.63e+02
Description	SAPAP2 protein.	SAPAP1 protein.	Human zona pellucida-	CDR2 from light chain	Tomato pZ130 cDNA-enc	Tomato ovary-specific	Humanised light	Humanised light	Light chain variable	Humanised light	Humanised light		Ovary tissue transcr:	pZ130 polypeptide	Mouse laminin A	Human leucocyte
QI	W69742	W69740	R74094	W27419	, R97559	W08364	W21854	W21855	W21844	W21853	W21848	W21852	R10310	R30779	W50891	W49219.
DB	34	34	14	.24	18	20	24	24	24	24	24	24	~	9	35	28
% Query Match Length DB	992	992	742	7	118	118	127	127	127	127	127	127	179	188	3084	15
% Query Match	92.3	92.3	89.7	87.2	87.2	87.2	87.2	87.2	87.2	87.2	87.2	87.2	87.2	87.2	87.2	84.6
Score	36	36	35	34	34	34	34	34	34	34	34	34	34	34	34	33
Result No.	-1	7	m	4	ഗ	ဖ	7	ω	O	10	11	12	13	14	15	16

# Page 1 SEG10; 7, 10,11,12 DO(1801704 山って

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35 277 277 37 38 38 38 38 38 38 38 38 38 38 38 38 38	7 11
	1021
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	
	2 11
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#### ALIGNMENTS

WPT: 98 47442241.

DNA encoding new animal protein SAPAP 2 - useful for diagnosis and treatment of nervous system diseases
Claim 1: Page 7-9: 11pp: Japanese.
Claim 1: Page 7-9: 11pp: Japanese.
The present sequence represents the SAPAP2 protein. Also described in the present invention is: (A) an animal protein having an amino acid sequence substantially the same as SAPAP2; (B) a CDNA sequence encoding the amino acid sequence of SAPAP2 or (C) an amino acid sequence by the above CDNA or its partial sequence. SAPAP2 is a new animal protein which combines specifically with PSD-95/SAP90 and its related protein and is useful for the diagnosis, prevention and treatment of various nervous diseases caused by functional or structural interference SAPAP2 protein.

Human; SAPAP2; SAPAP1; animal protein; PSD-95/SAP90; diagnosis;

Human; SAPAP2; SAPAP1; animal protein; PSD-95/SAP90; diagnosis;

mervous disease; functional interference; structural interference;

membrane associated guanylate kinase; neuronal disease.

Homo sapiens III0201428-A. 04-AUG-1998 24-JAN-1994-, 011715. 24-JAN-1997, JP-011715. (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN. (TAKE/) TAKEUCHI M. WPI; 98-474492/41. T W69742 standard; protein; 992 AA. (first entry) of nervous system. Sequence 992 AA; W69742; 26-OCT-1998 RESULT 

; 0 Score 36; DB 34; Length 992; Pred. No. 1.78e+02; 1; Mismatches 0; Indels 92.3%; ilarity 83.3%; Conservative Query Match Best Local Similarity Matches

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Gaps

402 hspklq 407 1 HSSKLQ 6 д οχ ~

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Nakamura K, Takatsu K;
WPI: 97-20249/18.
Antibody against alpha-chain of human interleukin 5 receptor --
useful for diagnosis and treatment of respiratory allergic diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                            e.g. chronic bronchitis
Claim 8; Page 165; 238pp; Japanese.
The present sequence is complementarity determining region 2 (CDR2)
from the light chain variable region of the murine anti-human
interleukin 5 receptor alpha chain (hIL-5R alpha) monoclonal
antibody (MAD) KM1259; KM1259 is produced by the hybridoma
FERM BP-5134, which was prepared by immunising Balb/c mice with
hIL-5R alpha, fusing spleen cells obtained from the mice with mouse
myeloma P3-01 cells and screening the resultant hybridomas. The MAD
can be used to detect or assay for hIL-5R alpha and cells
expressing it on their surface, especially to diagnose allergic
respiratory diseases, e.g. chronic bronchitis. It can also be used
                                                19-DEC-1997 (first entry)

CDR2 from light chain variable region of KM1259 antibody.

COMPLOADEMENTATILY determining region; CDR; light chain; treatment; variable region; murine; mouse; human; interleukin 5; IL-5; receptor; alpha chain; monoclonal antibody; hybridoma; detection; assay; diagnosis; allergic respiratory disease; chronic bronchitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-FDB5 '131023.

N-FDB5 '131023.

DNA construct for expressing melanin synthesis gene in plant ovule cells - contains promoter from the tomato p2130 gene, also binary vector and transgenic plants, esp. cotton, contg. construct

Example 3; Fig 1A-B; 25pp; English.

The tomato p2130 clone contains a 564 bp insert of cDNA (131823) detected only in a tomato cDNA library prepd. from pre-arthesis stage created for a protein (R87559) of unknown function. The clone was isolated from a library prepd. from cDNA of pre-anthesis stage ovaries. The p2130 transcriptional infitation region is considered to be ovary specific and can be utilised in DNA constructs for the expression of heterologous genes, partic. in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 34; DB 24; Length 7; Pred. No. 3.38e+02; 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ovary; ovule, fruit; tomato; cotton; melanin; vector;
                                                                                                                                                                                                                                                                                                (KYOW ) KYOWA HAKKO KOGYO KK.
Anazawa H, Furuya A, Hanai N, Iida A, Koike M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Martineau BM, Reilley AA, Stalker DM;
WPI; 96-308822/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R97559 standard; Protein; 118 AA.
14-58P-1996 (first entry)
Tomato pZ130 cDNA-encoded protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lycopersicon esculentum cv. UC82B. US5530185-A.
      W27419 standard; peptide; 7 AA. W27419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87.2%;
larity 66.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-JUN-1996.
19-JUL-1989; 382518.
19-JUL-1989; US-382518.
17-JUL-1992; US-554195.
29-DEC-1992; US-998158.
(CALJ ) CALGENE INC.
                                                                                                                                                                                                                                                 11-SEP-1996; JO2588.
11-SEP-1995; JP-232384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                      Mus spp.
WO9710354-A1.
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| HSSKLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ά
                                                                                                                                                                                                                                                                                                                                New protein SAPAPI - used for, e.g. diagnosis and prevention of various neuronal diseases

Claim 1 Page 4-7: 12pp; Japanese.

Claim 1 Page 4-7: 12pp; Japanese.

The present sequence represents the SAPAPI protein having a 992 amino acid (aa) sequence. Also described in the present invention are: (1) an animal protein having an aa sequence substantially homologous to SAPAPI. or an as sequence substantially homologous to SAPAPI, or an as sequence hybridised to the CDNA sequence. SAPAPI is a novel animal protein specific for PSD-95/SAP90 and its related protein, and may be useful for the diagnosis, prevention and treatment of various neuronal diseases caused
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The human zona pellucida-2 (HZP-2) protein may be used as a vaccine artigen. It can be artificially synthesised using recombinant techniques. Partial sequences of the HZP-2 gene were subcloned, the sequences and primers used in cloning and subcloning are given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                    76-74-1998 (first entry)
SAPAP1 protein.
Human; SAPAP1; SAPAP2; animal protein; PSD-95/SAP90; diagnosis;
nervous disease; functional interference; structural interference;
membrane associated guanylate kinase; neuronal disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A DNA coding human zona pellucida-2 protein - used as a vaccine
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36; DB 34; Length 992;
Pred. No. 1.78e+02;
1; Mismatches 0; Indels
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Pred. No. 2.46e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-JAN-1996 (first entry)
Human zona pellucida-2 (HZP-2) protein.
Human zona pellucida; HZP-2; protein; vaccine; antigen; contraceptive; ovary.
                                                                                                                                                                                                                      24-JAN-1997; 011714.
24-JAN-1999; DF-011714.
(RAGA-) RAGAKU GIJUTSU SHINKO JIGYODAN.
(TAKE/) TAKEUCHI M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 8-11; 11pp; Japanese.
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R74094 standard; Protein; 742 AA.
W69740 standard; protein; 992 AA. W69740;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92.3%;
Similarity 83.3%;
5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-APR-1995,
05-OCT-1993; 249404,
05-OCT-1993; JP-2494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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WPI; 95-182067/24.
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Best Local Similarity
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                                                                                                                                                          Homo sapiens.
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|HSSKLO
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Antibody against alpha-chain of human interleukin 5 receptor -
useful for diagnosis and treatment of respiratory allergic diseases,
e.g. chronic bronchitis

Example 2; Pages 157-158; 238pp; Japanese.
Che present sequence is the humanised light chain variable
region of the murine anti-human interleukin 5 receptor alpha chain
Chil-58 alpha monoclonal antibody (MAb) KM1259. KM1259 is produced
by the hybridoma FERM BP-5134, which was prepared by immunising
Balb/c mice with hiL-5R alpha, fusing spleen cells obtained from
the mice*with mouse myeloma P3-U1 cells and screening the resultant
thybridomas. The MAb can be used to detect or assay for hiL-5R alpha
and cells expressing it on their surface, especially to diagnose
allergic respiratory diseases.
Chemical control of the control of the mise of the control of the mise of the m
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2: Pages 160-161; 238pp; Japanese.
The present sequence is the humanised light chain variable region of the murine anti-human interleukin 5 receptor alpha chain (hll.5R alpha) monoclonal antibody (MAD) KM1259. KM1259 is produced by the hybridoma FERM BP-5134, which was prepared by immunising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-DEC-1997 (first entry)
Humanised light chain variable region of KM1259 antibody.
Complementarity determining region; CDR; light chain; treatment;
variable region; murine; mouse; human; interleukin 5; IL-5;
receptor; alpha chain; monoclonal antibody; hybridoma; detection;
assay; diagnosis; allergic respiratory disease; humanised;
chronic bronchitis; chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70..76
/label- complementarity_determining_region_2
109..117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44..54
/label= complementarity_determining_region_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= complementarity_determining_region_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 34; DB 24; Length 127;
Pred. No. 3.38e+02;
2; Mismatches 0; Indels
                                                                           Koike
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Koike
                                                                           Iida A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hanai N, Iida A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= sig_peptide
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/label= mat_peptide
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W21855 standard; Protein; 127 AA.
W21855;
                                                                           Hanai N,
                                             (KYOW ) KYOWA HAKKO KOGYO KK.
Anazawa H, Furuya A, Hanai N
Nakamura K, Takatsu K;
WPI; 97-202249/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (KYOW ) KYOWA HAKKO KOGYO KK
Anazawa H, Furuya A, Hanai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.28;
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Nakamura K, Takatsu K;
WPI; 97-202249/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric - Mus spp.
Chimeric - Homo sapiens.
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11-SEP-1996; J02588.
11-SEP-1995; JP-232384.
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Humanised light chain variable region of KM1259 antibody.
Homplementarity determining region; CDR; light chain; treatment; variable region; murine; mouse; human; interleukin 5; IL-5; receptor, alpha chain; monoclonal antibody; hybridoma; detection; assay; diagnosis; allergic respiratory disease; humanised; chronic bronchitis; chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA construct capable of directing ovary-tissue transcription in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plants - useful for modifying colour phenotype, in e.g. cotton Example 1; Fig 1; 75pp; English.

Novel polypeptides (W08364 and W08385) are respectively encoded by tomato p2130 (T48813) and p270 (T48814) ovary-specific genes. Their native function is unknown. The promoter regions of the genes can be used to direct ovary-specific transcription of a gene of interest in transgenic plants.
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/label= complementarity_determining_region_1
70..76
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/label= complementarity_determining_region_2
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                                                                      Length 118;
                                                                                                                                                                                                                                                                                                                                                    14-MAR-1997 (first entry).
Tomato ovary-specific p2130-encoded protein.
Ovary; fruit; colour; pigmentation; cotton; tomato; probe; promoter; p2130; p27; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 118;
                                             Score 34; DB 18; Length 110.
Pred, No. 3.386+02;
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Pred. No. 3.38e+02;
0; Mismatches 1;
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1.20
/label= sig_peptide
21..127
/label= mat_peptide
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W08364 standard; Protein; 118 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lycopersicon esculentum cv. W09640951-A2.
                                                                 Query Match 87.2%;
Best Local Similarity 83.3%;
Matches 5; Conservative
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Best Local Similarity 83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Conservative
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07-JUN-1996. U09911.
07-JUN-1995. US-487087.
(CALJ ) CALGENE INC.
MCBride K, Stalker DM;
WPI; 97-052341/05.
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Chimeric - Homo sapiens.
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early fruit development
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Sequence

Matches

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peptide peptide region region region

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Gaps

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region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antibody against alpha-chain of human interleukin 5 receptor - useful for diagnosis and treatment of respiratory allergic diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
Balb/c mice with hIL-5R alpha, fusing spleen cells obtained from the mice with mouse myeloma P3-U1 cells and screening the resultant hybridomas. The MAD can be used to detect or assay for hIL-5R alpha and cells expressing it on their surface, especially to diagnose allergic respiratory diseases, e.g. chronic bronchitis. It can also be used to treat such diseases.
                                                                                                                                                                                                                               Gaps
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Complementarity determining region; CDR; light chain; treatment; variable region; murine; mouse; human; interleukin 5; IL-5; receptor; alpha chain; monoclonal antibody; hybridoma; detection; assay; diagnosis; allergic respiratory disease; chronic bronchitis.
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/label= complementarity_determining_region_1
70.76
/label= complementarity_determining_region_2
109..117
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Pred. No. 3.38e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                  Length 127;
                                                                                                                                                             (KYOW ) KYOWA HAKKO KOGYO KK.
Anazawa H. Furuya A, Hanai N, Iida A, Koike
Nakamura K, Takatsu K;
WPI; 97-202249/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e.g. chronic bronchitis
Example 2; Pages 122-123; 238pp; Japanese.
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/label= sig_peptide
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/label= mat_peptide
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ilarity 66.7%;
Conservative
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66.7%;
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11-SEP-1995; JP-232384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treat such diseases.
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Best Local Similarity
Matches 4; Conser
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Best Local Similarity
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1 HSSKLQ (
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70 htsrlq |:|:|| 1 HSSKLQ

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" seful for diagnosis and treatment of respiratory allergic diseases,

" seful for diagnosis and treatment of respiratory allergic diseases,

" serion chanch bronchitis,

" Example 2: Pages 154-155; 238pp; Japanese.

" The present sequence is the humanised light chain variable

region of the murine anti-human interleukin 5 receptor alpha chain

(HIL-5R alpha) monoclonal anti-human interleukin 5 receptor alpha chain

(hIL-5R alpha) monoclonal anti-human interleukin 5 receptor alpha chain

(hIL-5R alpha) monoclonal anti-human interleukin 5 receptor alpha chain

(hIL-5R alpha) monoclonal anti-human spread by immunising

Balb/c mice with hIL-5R alpha, fusing spleen cells obtained from

" Balb/c mice with mouse myeloma 83-01 cells and screening the resultant

" hybridomas The MAb can be used to detect or assay for hIL-5R alpha

and cells expressing it on their surface, especially to diagnose

" allergic respiratory diseases, e.g. chronic bronchitis. It can also
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                                                                                        Humanised light chain variable region of KM1259 antibody.

Complementarity determining region; CDR; light chain; treatment;
variable region; murine; mouse; human; interleukin 5; IL-5;
receptor; alpha chain; monoclonal antibody; hybridoma; detection;
assay; diagnosis; allergic respiratory disease; humanised;
chronic bronchitis; chimeric.
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/label= complementarity_determining_region_1
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/label- complementarity_determining_region_2
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/label= complementarity_determining_region_3
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Pred. No. 3.38e+02;
Dred. man-tohes 0; Indels
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/label= sig_peptide
21..127
/label= mat_peptide
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Jr 10
W21853 standard; Protein; 127 AA.
W21853:
19-DEC-1997 (first entry)
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W21848 standard; Protein; 127 AA.
W21848;
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Sequence 127 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.7%;
Matches 4; Conservative
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Chimeric - Homo sapiens.
                                                                                                                                                                                                                                                         Chimeric - Mus spp.
Chimeric - Homo sapiens.
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Nakamura K, Takatsu K;
WPI; 97-202249/18.
N-PSDB: T73647.
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11-SEP-1995; JP-232
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|HSSKLQ
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                                                                                                                                                                                                                                                                                                                        Synthetic.
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23-JAN-1991.
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                                                                                                                                                                                                  Antibody against alpha-chain of human interleukin 5 receptor - useful for diagnosis and treatment of respiratory allergic diseases,
                                                                                                                                                                                                                      Example 2; Page 141; 238pp; Japanese.

The present sequence is the humanisad light chain variable region of the murine anti-human interleukin 5 receptor alpha chain (hIL-5R alpha) monoclonal antibody (MAD) KM1259. KM1259 is produced by the hybridoma FERN BP-5134, which was prepared by immunising the mice with hIL-5R alpha, fusing spleen cells obtained from the mice with hIL-5R alpha, fusing spleen cells obtained from the mice with mouse myebloma P3-U1 cells and screening the resultant hybridomas. The MAD can be used to detect or assay for hIL-5R alpha and cells expressing it on their surface, especially to diagnose allergic respiratory diseases, e.g. chronic bronchitis. It can also
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Humanised light chain variable region of KM1259 antibody.

Complementarity determining region; CDR; light chain; treatment; variable region; murine; mouse; human; interleukin 5; IL-5; receptor; alpha chain; monoclonal antibody; hybridoma; detection; assay; diagnosis; allergic respiratory disease; humanised; chronic bronchitis; chimeric.
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                                         /label= complementarity_determining_region_1 70..76 /label=_complementarity_determining_region_2
                                                                          4..54
|abel= complementarity_determining_region_1
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Pred. No. 3.38e+02;
2; Mismatches 0; Indels
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                                                                                                                                            (KYOW ) KYOWA HAKKO KOGYO KK.
Anazawa H, Furuya A, Hanai N, Iida A,
Nakamura K, Takatsu K;
/label= sig_peptide
21..127
/label= mat_peptide
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1abel= mat_peptide
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W21852 standard; Protein; 127 AA.
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Sest Local Similarity 66.7%;
Aatches 4; Conservative
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Chimeric - Homo sapiens.
                                                                                                                        11-SEP-1996; J02588.
11-SEP-1995; JP-232384.
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11-SEP-1995; JP-232384.
                                                                                                                                                                   Nakamura K, Takat;
WPI; 97-202249/18.
                                                                                                                                                                                                                                                                                                                                                              127 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                              70 htsrlg 75
                                                                                                                                                                                         N-PSDB; T73631
                                                                                                                                                                                                                                                                                                                                                                                                                                         |:|:||
1 HSSKLO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9710354-A1.
                                                                                                             20-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
          peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New ovary tissue transcriptional factors - modify transcription in tomato plant ovaries for use as mol. probes bisclosure; Fig 1, 21pp; English.

The tomato-derived transcriptional initiation region which regulates the expression of the sequence corresp. to the p2130 clone is considered ovary-specific. Sequences hybridisable to the p2130 clone, e.g. probe p27, show abundant mRNA, esp. at the early stages of anthesis. The message is expressed in ovary integument and ovary outer pericarp tissue and is not expressed, or at least not readily detectable, in other tissues or at any other stage of fruit
                                                                                                                                                        Example 2: Pages 151-152; 238pp; Japanese.

The present sequence is the humanised light chain variable region of the murine anti-human interlaukin 5 receptor alpha chain (hiL-5R alpha) monoclonal antibody (MAb) KM1259. KM1259 is produced by the hybridoma FERM BP-5134, which was prepared by immunising Balb/C mice with hiL-5R alpha, fusing spleen cells obtained from the mice with mouse myeloma B3-dI cells and screening the resultant hybridomas. The MAb can be used to detect or assay for hiL-5R alpha and cells expressing it on their surface, especially to diagnose allergic respiratory diseases, e.g. chronic bronchitis. It can also be used to treat such diseases.
                                                                            Antibody against alpha-chain of human interleukin 5 receptor - useful for diagnosis and treatment of respiratory allergic diseases, e.g. chronic bronchitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ovary tissue transcriptional factor DNA clone p2130 product. Ovary tissue transcriptional factor; DNA construct; probe:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            development. The native function of the amino acid sequenc
encoded by the structural gene comprising pZ130 is unknown.
See also Q10263-64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 179;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 34; DB 24;
Pred. No. 3.38e+02;
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Pred. No. 3.38e+02;
0; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .n 13
10.1310 standard; Protein; 179 AA.
R10310;
04-APR-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JT 14
R30779 standard; Protein; 188 AA.
R30779;
19-MAY-1993 (first entry)
pZ130 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lycopersicon esculentum UC82B.
EP-409629-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87.2%;
larity 66.7%;
Conservative
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Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-JUL-1990; 307926.
19-JUL-1989; US-382518.
(CALG-) CALGENE INC.
Takatsu K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Martineau B, Houck CM;
WPI; 91-024191/04.
N-PSDB; Q10262.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
            WPI; 97-202249/18.
N-PSDB; T73644.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 htsrlq 75
|:|:||
1 HSSKLQ 6
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US-09-081-707-7.rag

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disease or CJD
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                            Region
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o
cDNA; clone p2130; anthesis; tomato; ovary; integumen; outer pericarp; fruit; developement; transcription; initiation; region; modulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence represents the polypetide of cDNA clone pz130. This sequence is expressed during the early stages of anthesis in tomatos. The message is expressed in ovary integumen and ovary outer pericarp tissue. It is not readily detectable in other tissues or at other stages of fruit developement. The transcription initiation region associated with this gene is therefore considered to be ovary specific. The actual function of the pz130 polypeptide is unknown. The transcription initiation region can be used for modulation of endogenous fruit products, for production of exgenous products and for modification of the phenotype of fruit and fruit products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Down's syndrome; hereditary cerebral haemorrhage; inflammation; malignancy; Familial Mediterranean Fever; multiple myeloma; type II dlabetees; prion disease; Creutzfeldt-Jacob disease; CJD; Gertstmann-Straussler syndrome; kuru; scrapie; haemodialysis; carpal tunnel syndrome; senile cardiac amyloid polyneuropathy; Familial Amyloidotic Polyneuropathy; thyroid carcinoma; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA constructs contg. tomato p2130 transcriptional initiation region - useful for modulation of endogenous fruit prods. and for prodn. of exogenous prods.
                                        ovary-specific; endogenous; fruit product; exogenous; phenotype. Lycopersicon esculentum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-DEC-1998 (first entry)
Mouse laminin A chain.
Laminin; mouse; beta-amyloid; amyloidosis; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 34; DB 6; Length 188; Pred. No. 3.38e+02;
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                                                                                                                                      /note= "Nonsense codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "Nonsense codon"
                                                                                                                                                                                   /note= "Nonsense codon"
                                                                                                                                                                                                                                                                                                                                                                       /note= "Nonsense codon"
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2746..2922
                                                                                        Location/Qualifiers
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W50891 standard; Protein; 3084 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 1; 18pp; English.
                                                                                                                                                                                                                                                                                                                            'note= "Nonsense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUL-1989; US-382518.
17-JUL-1990; US-554195.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CALJ ) CALGENE INC.
Houck CM, Martineau BM;
WPI; 93-026940/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                misc_difference 120
                                                                                                                                                                                                      misc_difference 126
                                                                                                                                                                                                                                                                                                                                                                                            misc_difference 160
                                                                                                                   misc_difference 119
                                                                                                                                                                                                                                                    misc_difference 129
                                                                                                                                                                                                                                                                                                                                               misc_difference 152
                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_difference 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188 AA;
                                                                                                                                                                                                                                                                                                    misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; 034940.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 hcsklq 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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Dp
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disease or Cap.

This is the amino acid sequence of the mouse laminin, laminin-derived principle. This is the amino acid sequence of the mouse laminin, laminin-derived principle. This is the amino acid sequence of the mainin derived protein fragments and/or laminin-derived polypeptides as potent inhibitors of amyloid formation, deposition, accumulation and/or persistence in Alzheimer's disease and other amyloidoses. The laminin products (see W5088-98) may include mouse or human laminin products (see W5088-98) may include mouse or human laminin a or Lohain, laminin Bl or B2 chain, laminin A2 chain (merosin), laminin bl or B2 chain, laminin A chain and the beta-amyloid binding domain of the laminin A2 chain (merosin), laminin protein. A method for disease comprises administering a polypeptide having a conformational similarity to a fragment of a laminin protein. A method for diamonin in a sample. Production of laminin or its fourth globular repeat in vivo provides a method for laminin or its fourth globular repeat in vivo provides a method for laminin or its fourth globular repeat in vivo provides a method for laminin or its fourth globular repeat in vivo provides a method for laminin or its fourth globular repeat in vivo provides a method for laminin or its fourth globular repeat in vivo provides a method for laminin or its fourth globular repeat in vivo provides and treatment of amyloidosis, protein, virial manition or sansociated with chronic inflammation, various forms of malignancy and Familial Mediterranean Fever (AA amyloid), the amyloidosis associated with type II diabetes associated with multiple myloid), the amyloidosis associated with home of the manitial Amyloidosis associated with seriod and Familial Amyloidosis associated with endocrine tumours such as medullary carcinome of procalcitonin).

Second the provide of procalcitonin).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of laminin and fragments - for developing products for use in the diagnosis and treatment of amyloid disease, e.g. Alzheimer's
/note= "fourth globular domain repeat (Claim 13)"
2690..2700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                DB 35; Length 3084;
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0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: Thu Oct 28 11:19:48 1999
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Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                            16-APR-1998.
08-OCT-1997; U18145.
08-OCT-1996; US-027981.
(UNIW ) UNIV WASHINGTON.
                                                                                                                                                                                                                                                                                                                                                                                      castillo G, Snow AD;
WPI; 98-240534/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1764 hseklq 1769
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Oct 28 11:20:06 1999; MasPar time 2.92 Seconds 82.440 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-081-707-7 (1-6) from US09081707.pep 39 Description: Perfect Score:

Sequence:

1 HSSKLQ 6

122810 seqs, 40068593 residues Searched:

PAM 150 Gap 15

Scoring table:

Post-processing: Minimum Match 0% Listing first 45 summaries

pir60 1:pir1 2:pir2 3:pir3 4:pir4 Database:

scale 1.195 Mean 17.857; Variance 14.939; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		dР					
	Score	Query	Length	DB	ID	Description	Pred. No.
	39	100.0	147	7	\$13157	hemoglobin - polychae	1.546+00
	39	100.0	582	7	A43412	_	1.546+00
	37	94.9		7	E65011		5.99e+00
	37	94.9	278	7	н65069		5.99e+00
	37	94.9	883	~	A71434		5.99e+00
	36	92.3	147	~	B36529	hemoglobin P3 - polvc	1.16e+01
	36	92.3	808	~	T01344	pro	1,16e+01
	36	92.3	531	~	B54096	flavin-containing mon	1.16e+01
	36	92.3	533	Н	S18380	dimethylaniline monoo	1.16e+01
	36	92.3	675	m	T00013	DAP-1 beta protein -	1.16e+01
	36	92.3	692	7	T00025	PSD-95 binding protei	1.16e+01
	36	92.3	744	~	S45060	outer capsid spike pr	1.16e+01
	36	92.3	744	7	S45061	outer capsid spike pr	1.16e+01
	36	92.3	977	m	T00014	DAP-1 alpha protein -	1.16e+01
	32	89.7	2067	7	A42854	probable spindle pole	2.21e+01
	34	87.2		~	857809	gamma-thionin-like pr	4.14e+01
17	34	87.2		7	A36529	hemoglobin P2 - polyc	4.14e+01
	34	87.2		7	S63532	ne	4.14e+01
_	34	87.2	294	7	S58472 ·		4.14e+01
_	34	87.2		~	T02574	hypothetical protein	4.14e+01
	34	87.2		7	G64220	ATP-binding protein m	4.14e+01
	34	87.2	1377	7	A38926	DNA-binding protein c	4.14e+01
	34	87.2	3084	Н	MMMSA	laminin alpha-1 chain	4.14e+01
						•	

ö A43412 #type complete semenogelin II precursor - human #formal\_name Homo sapiens #common\_name man 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 22-May-1998 A43412; B31489; A45295; S29156; S68765; S68762 Gaps #superiamily globin; globin homology #length 147 #molecular-weight 16029 #checksum 7221 ; 0 Query Match
100.0%; Score 39; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 1.54e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 57 HSSKLQ 62 1 HSSKLQ 6 CLASSIFICATION SUMMARY ~ ENTRY TITLE ORGANISM DATE RESULT

q QΥ

#authors Ulvsback, M.; Lazure, C.; Lilja, H.; Spurr, N.K.; Rao, V.V.;
Loffler, C.; Hansmann, I.; Lundwall, A.

#journal J. Biol. Chem. (1992) 267:18080-18084

#title Gene structure of semenogelin I and II. The predominant proteins in human semen are encoded by two homologous genes #cross-references MUID:92388176 ACCESSIONS REFERENCE

#accession

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Query Match
Best Local Similarity
                                                                                                                               230 HSSKLQ 235
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                                                                                                                          ERENCE A31489
#authors Lilja, H.; Abrahamsson, P.A.; Lundwall, A.
#authors J. Biol. Chem. (1989) 264:1894-1900
#title Semenogelin, the predominant protein in human semen. Primary structure and identification of closely related proteins in the male accessory sex glands and on the spermatozoa.
#cross-references MUID:89109218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     this report is of a secondary sequence determined simultaneously with the sequence with accession number $20155 (see entry WTHUB); as a secondary sequence, it should be considered less than fully reliable
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##molecule_type protein
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Isolation and characterization of the major gel proteins in
human semen, semenogelin I and semenogelin II.
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Malm, J.; Hellman, J.; Magnusson, H.; Laurell, C.B.; Lilja,
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#product semenogelin II #status predicted #label MAT\
#binding_site carbohydrate (Asn) (covalent) #status
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##residues 390,'E',392-396,'E',398-400,'EW',403-405,'C',407,'DE'
##label SCH
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repeat
##molecule_type DNA
#residues
1-582 ##label ULV
##cross-references GB:M81651; NID:g307417; PID:g307418
##cross-references GB:M81651; NID:g307417; PID:g307418
##note
NCBIP:112889)
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Bur. J. Biochem. (1996) 238:88-96
Characterization of semenogelin II and its molecular
interaction with prostate-specific antigen and protein
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Schneider, K.; Kausler, W.; Tripier, D.; Jouvenal, K.;
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#journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:4559-4563
#title Molecular cloning of epididymal and seminal vesicular transcripts encoding a semenogelin-related protein.
#cross-references_MUID:92262479
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##residues 214-278,'Y',280-281 ##label LIL
SNCE A45295
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##residues 420-421,'G',423-423 ##label
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##residues 3-582 ##label LI2
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Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao,
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##cross-references GB:AE000326; GB:U00096; NID:g1788718; PID:g2367134;
##CP:b2376
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| 1-778 ##label BLAT
| #cross-references GB:AE000369; GB:U00096; NID:g2367168; PID:g1789227;
| UWGP:b2863
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#formal_name Escherichia coli
12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change
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Score 39; DB 2; Length 582;
Pred. No. 1.54e+00;
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Pred. No. 5.99e+00;
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T01344 #type complete
hypothetical protein F6N15.5 - Arabidopsis thaliana
#formal_name Arabidopsis thaliana #common_name mouse-ear
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##molecule_type mRNA
##residues 1-147 ##label ZAF
##cross-references GB:M55444; GB:U05691; NID:9159146; PID:9159147
CLASSIFICATION #superfamily globin; globin homology
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                                                                                                            #domain globin homology #label GLB
#length 147 #molecular-weight 15977 #checksum 8871
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##molecule_type DNA
##rosiance
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Pred. No. 1.16e+01;
''' matches 0; Indels
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submitted to the EMBL Data Library, May 1998
The sequence of A. thaliana F6N15.
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#accession B54096
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Dean, C.; Bergkamp, R.; Dirkse, W.; Van Staveren, M.;
Stiekema, W.; Drost, L.; Ridley, P.; Hudson, S.A.; Patel,
K.; Murphy, G.; Piffanelli, P.; Wedler, H.; Wedler, E.;
Galen, J.; Villarroel, R.; Peoll, T.M.; Terryn, N.;
Giclen, J.; Villarroel, R.; De Clerck, R.; Van Montagu, M.;
Lecharny, A.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger,
M.; Schaeffer, M.; Funk, B.; Mueller-Auer, S.; Silvey, M.;
James, R.; Montfort, A.; Pons, A.; Puigdomenech, P.; Douka,
A.; Voukelatou, E.; Milioni, D.; Hatzopoulos, P.;
Piravandi, E.; Obermaier, B.; Hilbert, H.; Duesterhoft, A.;
Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.;
Rechman, S.; Ansorge, W.; Cooke, R.; Berger, C.; Delseny,
M.; Voet, M.; Volckaert, G.; Mewes, H.W.; Klosterman, S.;
Schueller, C.; Chalwatzis, N.
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#title Analysis of 1.9 Wh of contiguous sequence from chromosome 4
cof Arabidopsis thaliana.
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J. Biol. Chem. (1990) 265:21843-21851
The cDNA sequences encoding two components of the polymeric fraction of the intracellular hemoglobin of Glycera
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#formal_name Glycera dibranchiata #common_name bloodworm
12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change
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probable RNA helicase - Arabidopsis thaliana
#formal_name Arabidopsis thaliana #common_name mouse-ear
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*superfamily dimethylaniline monooxygenase (N-oxide-forming) oxidoreductase #length 531 #molecular-weight 59815 #rharkeim Ross
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J. Blol. Chem. (1994) 269:14314-14322
Cloning and sequencing flavin-containing monooxygenases
FMO3 and FMO4 from rabbit and characterization of FMO3.
                                                                                 Gaps
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Score 36; DB 2; Length bus;
Pred. No. 1.16e+01;
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##cross-references GB:L10391; NID:g349533; PID:g349534
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Okumura, N.; Matsumine, A.; Kobayashi, S.; Toyoshima, K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##molecule_type protein
##residues 1-32 ##label OZO2
##residues 1-32 ##label OZO2
NT This enzyme is involved in the metabolism of many drugs,
pesticides, and other foreign compounds, including xenobiotics,
by catalyzing the NADPH-dependent oxidation of various
substrates.
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                                                                                                                                                                           dimethylaniline monooxygenase (N-oxide-forming) (EC 1.14.13.8), hepatic 2 - rabbit dimethylaniline oxidase; flavin-containing monooxygenase #formal_name Oryctolagus cuniculus #common_name domestic
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kinase-like domains of hDLG and PSD-95.
T00013
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#journal Arch. Biochem. Biophys. (1991) 290:103-115
#title Multiple forms of liver microsomal flavin-containing monoxygenases: complete covalent structure of form 2.
#cross-references MUID:91378577
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#formal_name Homo sapiens #common_name man
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Differential expression of isoforms of PSD-95 binding protein (GKAP/SAPAP1) during rat brain development.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kawashima, N.; Takamiya, K.; Sun, J.; Kitabatake, A.; Sobue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                 T00025 #type complete
PSD-95 binding protein - rat
#formal_name Rattus norvegicus #common_name Norway rat
22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change
22-Jan-1999
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##cross-references EMBL:AB003594; NID:d1177606; PID:d1025176

"X #hength 692 #molecular-weight 76991 #checksum 9411
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##cross-references EMBL:X79441; NID:9495228; PID:9495229
FICATION #superfamily rotavirus outer layer protein VP3
X Hength 744 #molecular-weight 84036 #checksum 6403
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                                                                                                                               Length 675;
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Pred. No. 1.16e+01;
1; Mismatches 0
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##residues 1-692 ##label KAW
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Molecular cloning, complete nucleotide sequence and coding assignment of the outer capsid spike protein (VP4) from a human group C rotavirus: comparison with th VP4 gene of a brazilian isolate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Satoh, K.; Yanai, H.; Senda, T.; Kohu, K.; Nakamura, T.; Okumura, N.; Matsumine, A.; Kobayashi, S.; Toyoshima, K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genes to Cells (1997) 2:415-424
DAP-1, a novel protein that interacts with the guanylate kinase-like domains of hDLG and PSD-95.
                                       13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change .08-Sep-1997 845061 845060
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probable spindle pole body component bimB - Emericella
nidulans
cell division-associated protein bimB
#formal name Emericella nidulans, Aspergillus nidulans
10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change
10-Oct-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DAP-1 alpha protein - human
#formal_name Homo sapiens #common_name man
19-Jan-1999 #sequence_revision 19-Jan-1999 #text_change
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May, G.S.; McGoldrick, C.A.; Holt, C.L.; Denison, S.H.
J. Biol. Chem. (1992) 267:15737-15743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##status preliminary
##residues 1-977 ##label SAT
##cross_references Emil 250277; NID:d1173042; PID:d1024135
##cross_references PAT #molecular~weight 108872 #checksum 4168
                                                                                                                                                                                                                                                                                             ##residues 1-744 ##label FIE ##cross-references EMBL:X79442; NID:9495230; PID:9495231 ##cross-references EMBL:X79442; NID:9495230; PID:9495231 FICATION #superfamily rotavirus outer layer protein VP3 #length 744 #molecular-weight 84080 #checksum 8279
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##residues 1-2010, PLSIG', 2016 ##label MA2 #cross-references EMBL:M83232; NID:9168020; PID:9168021 ##note this sequence differs by a frameshift after residue 2010
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May, G.S.; McGoldrick, C.A.; Denison, S.H.; Holt, C.L. submitted to the EMBL Data Library, February 1992 The binB3 mutation of Aspergillus nidulans uncouples DNA replication from the completion of mitosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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##molecule_type DNA
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Oct 28 11:20:37 1999; MasPar time 2.03 Seconds 83.380 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-081-707-7 (1-6) from US09081707.pep 39 1 HSSKLQ 6 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

77977 seqs, 28268293 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

swiss-prot37 1:swissprot Database:

Mean 18.322; Variance 13.214; scale 1.387 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Pred. No.	3.93e-01	3.93e-01	3.93e-01	3.93e-01	1.81e+00	3.80e+00	3.80e+00	3.80e+00	7.83e+00	1.58e+01	1.58e+01	1.58e+01	1.58e+01	1.58e+01	1.58e+01	1.58e+01	3.15e+01	3.15e+01	3.15e+01	3.15e+01	3.15e+01	3.15e+01	3.15e+01
Description	GLOBIN, MAJOR POLYMERI	PEROXISOME ASSEMBLY PR	SEMENOGELIN II PRECURS	SEMENOGELIN II PRECURS	HYPOTHETICAL 10.2 KD L	GLOBIN, POLYMERIC COMP	DIMETHYLANILINE MONOOX	DYSTROPHIN-RELATED PRO	CELL DIVISION-ASSOCIAT	GLOBIN, POLYMERIC COMP	PROBABLE TRNA (5-METHY	HYPOTHETICAL ABC TRANS	CUBITUS INTERRUPTUS DO	HYPOTHETICAL PROTEIN K	MYOSIN IJ HEAVY CHAIN.	LAMININ ALPHA-1 CHAIN	KRUEPPEL HOMOLOGOUS PR	HEMOGLOBIN BETA CHAIN.	40S RIBOSOMAL PROTEIN	40S RIBOSOMAL PROTEIN	HYPOTHETICAL 20.1 KD P	ECDYSONE-INDUCED PROTE	HYPOTHETICAL 30.6 KD P
di di	GLP1_GLYDI	PEX2_YARLI	SEM2_HUMAN	SEM2_MACMU	YPDI_ECOLI	GLP3_GLYDI	FMO3_RABIT	DRP2_HUMAN	BIMB_EMENI	GLP2_GLYDI	TRMU_SCHPO	Y187_MYCGE	CID_DROME	Y133_HUMAN	MYSJ_DICDI	LMA1_MOUSE	KRUH_DROME	HBB_RANES	R11B_ARATH	R11A_ARATH	Y053_SYNY3	E128_DROME	YM92_YEAST
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#### ALIGNMENTS

RESULT	LT 11
ΙD	GLP1_GLYDI STANDARD; PRT; 147 AA.
AC	
DT	(REL. 20, CREAT
DI	(REL. 20, LAST
DT	01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)
DE	GLOBIN, MAJOR POLYMERIC COMPONENT P1.
SO	GLYCERA DIBRANCHIATA (BLOODWORM).
ပ္ပ	EUKARYOTA; METAZOA; ANNELIDA; POLYCHAETA; PHYLLODOCIDA; GLYCERIDAE;
8	GLYCERA.
RN	
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 1-27; 98-102 AND 119-145.
RX	MEDLINE; 91091412.
RA	ZAFAR R.S., CHOW L.H., STERN M.S., VINOGRADOV S.N., WALZ D.A.;
RI	"The heterogeneity of the polymeric intracellular hemoglobin of
RT	Glycera dibranchiata and the cDNA-derived amino acid sequence of one
RT	component.";
RL	BIOCHIM. BIOPHYS. ACTA 1041:117-122(1990).
ပ္ပ	-!- SUBUNIT: POLYMER.
ပ္ပ	-!- THIS PROTEIN IS ONE OF AT LEAST SIX COMPONENTS IN THE POLYMERIC
႘	FRACTION OF GLYCERA HEMOGLOBIN.
ပ္ပ	
ပ္ပ	This SWISS-PROT entry is copyright. It is produced through a collaboration
ပ္ပ	between the Swiss Institute of Bioinformatics and the EMBL outstation -
ខ	the European Bioinformatics Institute. There are no restrictions on its
ပ္ပ	use by non-profit institutions as long as its content is in no way
ខ	modified and this statement is not removed. Usage by and for commercial
ပ္ပ	entities requires a license agreement (See http://www.isb-sib.ch/announce/
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DR	EMBL: X54060; G9347;
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DR	PROSITE: PS01033; GLOBIN: 1.
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no	100.0%; Score 39;
Be	Pred. No. 3.93e-01 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE-SEMINAL VESICLE;
TESCOF-SEMINAL VESICLE;
LUNDWALL A., LILJA H.;
"Molecular, cloning of epididymal and seminal vesicular transcripts
                                                                                                                                                                                                                                                                                          SZILARD R.K., RACHUBINSKI R.A.;
"The Yarrowia lipolytica gene PAY5 encodes a peroxisomal integral
membrane protein homologous to the mammalian peroxisome assembly
                                                                                                                                                     YARROWIA LIPOLYTICA (CANDIDA LIPOLYTICA).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
DIPODASCACEAE; YARROWIA.
                                                                                                                                                                                                                                                                                                                                                                        .
0
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASP/GLU-RICH (HIGHLY ACIDIC).
POLY-GLU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                          EITZEN G.A., TITORENKO V.I., SMITH J.J., VEENHUIS M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
-!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 39; DB 1; L. Pred. No. 3.93e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLY-ASP.
489F7120 CRC32;
                                                                       01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
PEROXISOME ASSEMBLY PROTEIN PAYS (PEROXIN-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
SEMENOGELIN II PRECURSOR (SGII).
                  380 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            582 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
POTENTIAL.
C3HC4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PSO0518; ZINC_FINGER_C3HC4; 1. PFAM; PF00097; Zf-C3HC4; 1. IRANSMEMBRANE; PEROXISOME: ZINC-FINGED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLY-GLY.
                  PRT;
                                                     01-NOV-1997 (REL. 35, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42727 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U43081; G1209744; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       380 AA;
                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE; 96355353.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92 HSSKLQ 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |||||||
| HSSKLQ 6
                                                                                                                                                                                                                                                                                                                                                       factor PAF-1
                                                                                                                                  PEX2 OR PAY5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEM2_HUMAN
Q02383;
                PEX2_YARLI
099155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
ZN_FING
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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RESULT
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between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                       -i- SUBUNIT: DISULFIDE-LINKED COMPLEXES OF SEMENOGELIN I AND THE OTHER SEMENOGELIN PROTEINS, THE 71- AND 76-KD POLYPEPTIDES.
-i- TISSUE SPECIFICITY: SEMINAL VESICLES, AND TO A MUCH LESSER
                                                                                   EXTENT, EPIDIDYMIS.
-1- PIM: SEMENOGELIN II IS THOUGHT TO FORM BOTH THE 71-KD POLYPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EUKARYOTA; METAZOA; CHORDATÀ; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; CERCOPITHECIDAE; CERCOPITHECINAE; MACACA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2-2.
4 X 60 AA TANDEM REPEATS, TYPE I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
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Pred. No. 3.93e-01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         AND, IN ITS GLYCOSYLATED FORM, THE 76-KD POLYPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEMEN; SEMINAL VESICLE; REPEAT; SIGNAL; GLYCOPROTEIN.
encoding a semenogelin-related protein.";
PROC. NATL. ACAD. SCI. U.S.A. 89:4559-4563(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEMENOGELIN II.
REPEAT-RICH REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROBABLE.
DD20304E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-UL-1998 (REL. 36, LAST ANNOTATION UPDATE)
SEMENOGELIN II PRECURSOR (SGII).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          706 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MACACA MULATTA (RHESUS MACAQUE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
llarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M81651; G307418; -.
EMBL; M81652; G338239; -.
EMBL; Z47556; E82662; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      559
200
200
260
559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A43412; A43412.
MIM; 182141; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          582 AA;
                                                   N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE; 97274635.
                                                                           MEDLINE; 92388176.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230 HSSKLQ 235
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1 HSSKLQ 6
                                     [2]
SEQUENCE FROM
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9
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SEM2_MACMU
Q95196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
REPEAT
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
REPEAT
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US-09-081-707-7.rsp

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Gaps

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Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1993 (REL. 27, CREATED)
01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
01-FBE-1996 (REL. 33, LAST ANOTATION UPDATE)
101-FBE-1996 (REL. 33, LAST ANOTATION UPDATE)
101-FBE-1996 (REL. 31, LAST ANOTATION UPDATE)
(HEPATIC FLAVIN-CONTAINING MONOOXYGENASE 3) (FMO 3) (DIMETHYLANILINE
OXIDASE 3) (FMO 1D1) (FMO FORM 2).
                                                                                                                                                                                                                                                                                                                                                        EUKARYOTA; METAZOA; ANNELIDA; POLYCHAETA; PHYLLODOCIDA; GLYCERIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORYCTOLAGUS CUNICULUS (RABBIT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
LAGOMORPHA; LEPORIDAE; ORYCTOLAGUS.
    Pred. No. 1.81e+00;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36; DB 1; Le
Pred. No. 3.80e+00;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEME; OXYGEN TRANSPORT; RESPIRATORY PROTEIN.
SEQUENCE 147 AA; 15977 MW; 747D26B7 CRC32;
                                                                                                                                                                                                                                         01-MAY-1991 (REL. 18, CREATED)
01-MAY-1991 (REL. 18, LAST SEQUENCE UPDATE)
01-NOV-1991 (REL. 20, LAST ANNOTATION UPDATE)
GLOGELN, POLYMERIC COMPONENT P3.
GLYCERA DIBRANCHIATA (BLOODWORM).
                                                                                                                                                                                                     147 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              530 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 94245761.
BURNETT V.L., LAWTON M.P., PHILPOT R.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-NEW ZEALAND WHITE; TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRACTION OF GLYCERA HEMOGLOBIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, M55444; G159147; -.
PIR; B36529; B36529.
PROSITE; PS01033; GLOBIN; 1.
PFRM; PF00042; Globin; 1.
HSSP; P02216; 1HBG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92.3%;
larity 83.3%;
Conservative
      larity 83.3%;
Conservative
                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
  Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 91072390.
                                                                      HSTKLQ 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
                                                                                                            1 HSSKLQ 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                            LT 6
GLP3_GLYDI
P21660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 HNSKLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FMO3_RABIT
P32417;
                                                                                                                                                                                                                                                                                                                                                                            GLYCERA.
                                                                      48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
O
                                                          and baboon.";
EUR. J. BIOCHEM. 245:25-31(1997).
-!- FUNCTION: PARTICIPATE IN THE FORMATION OF A GEL MATRIX ENTRAPPING
-!- FUNCTION: PARTICIPATE IN THE FORMATION OF A GEL MATRIX ENTRAPPING
-!- FUNCTION: PARTICIPATE IN THE ACCESSORY GLAND SECRETIONS AND EJACULATED SPERMATOZOA.

THE ACCESSORY GLAND SECRETIONS AND EJACULATED SPERMATOZOA.
                    "Cloning of the semenogelin II gene of the rhesus monkey.
Duplications of 360 bp extend the coding region in man, rhesus monkey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=K12 / MG1655;
MEDLINE: 97426617.
BLATTNER F.R., PUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,
RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,
GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
MAU B., SHAO Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-DEC-1998 (REL. 37, CREATED)
15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
HYPOTHETICAL 10.2 KD LIPOPROTEIN IN EVGS-DDG REGION PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The complete genome sequence of Escherichia coli K-12.";
SCIENCE 277:1453-1474(1997).
-!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL LIPOPROTEIN YPDI. N-ACYL DIGLYCERIDE (POTENTIAL). 294E168F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39; DB 1; Length 706; Pred. No. 3.93e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 91;
                                                                                                                                                                                                                                                                                                                                               EMBL; X92589; E208370; -.
SEMEN; SEMINAL VESICLE; REPEAT; SIGNAL; GLYCOPROTEIN.
SIGNAL 1 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; ABUULLE, POUR PROKENTINGE TO PROSITE; PS00013; PROKENTITOPROTEIN; 1.
HYPOTHETICAL PROTEIN; MEMBRANE; LIPOPROTEIN; SIGNAL.
18 POTENTIAL.
18 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                     706 AA; 79875 MW; 9D5897A8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                     SEMENOGELIN II
                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10162 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE000326; G2367134; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
ULVSBACK M., LUNDWALL A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANCHOR (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234 HSSKLQ 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 HSSKLQ 6
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ID YPDI_ECOLI
AC 032528;
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Matches

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Gaps

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HDD PT THE SECOND COLOR COLOR

Length 147; 0; Indels

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                                                                                                                                                                                                                          MEDLINE; 96225452.

ROBERTS R.G., FREEMAN T.C., KENDALL E., VETRIE D.L.P., DIXON A.K., SHAW-SMITH C., BONE O., BOBROW M.;

"Characterization of DRP2, a novel human dystrophin homologue.";

NAT. GENET. 13:223-226(1996).

-I- FUNCTION: POSSIBLY INVOLVED IN MEMBRANE-CYTOSKELETON INTERACTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=A773;
MEDLINE; 92348436.
MAY G.S., MCGOLDRICK C.A., HOLT C.L., DENISON S.H.;
"The bimB3 mutation of Aspergillus nidulans uncouples DNA replication from the completion of mitosis.";
J. BIOL. CHEM. 267:15737-15743(1992).
                                                                                                                                                                                                                                                                                                                                                                                          OF THE CENTRAL NERVOUS SYSTEM.
--- TISSUE SPECIFICITY: BRAIN AND SPINAL CORD; VERY LOW LEVELS IN EYE OVARY, EPIDIDYMIS AND TESTIS; NOT IN CARDIAC AND SKELETAL MUSCLE.
--- SIMILARITY: IN OVERALL STRUCTURE TO DP116 DYSTROPHIN ISOFORM.
                                                                           HOMO SAPIENS (HUMAN).
EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMERICELLA NIDULANS (ASPERGILLUS NIDULANS).
EUKARYOTA; FUNGI; ASCOMYCOTA; EUASCOMYCETES; PLECTOMYCETES;
EUROTIALES; TRICHOCOMACEAE; EMERICELLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36; DB 1; Length 954; Pred. No. 3.80e+00; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.
WW DOMAIN.
ZZ DOMAIN.
TO EF-HAND.
TO EF-HAND.
W, 0197AA02 CRC32;
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(REL. 27, LAST SEQUENCE UPDATE)
(REL. 28, LAST ANNOTATION UPDATE)
  01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) DYSTROPHIN-RELATED PROTEIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 2067 AA
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31 SITE I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92.3%;
llarity 83.3%;
Conservative
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380
648
451
500
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CA_BIND 20
REPEAT 98 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
                                                                                                                                                                               FROM N.A.
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01-0CT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1994
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                                                                                                                                                                                  SEQUENCE
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     ID DAT DOT DOT DOT SERVICE SER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMEL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                       "Liver microsomes contain two distinct NADPH-Monooxygenases with NH2-terminal segments homologous to the flavin containing NADPH-monooxygenase of Pseudomonas fluorescens."; BLOCHEM. BIOPHYS. RES. COMMUN. 163:49-55(1989).

-!- FUNCTION: THIS PROTEIN IS INVOLVED IN THE OXIDATIVE METABOLISM OF A VARIETY OF XENOBIOTICS SUCH AS DRUGS AND PESTICIDES. FORM II N-OXYGENATES PRIMARY ALIPHATIC ALKYLAMINES AS WELL AS SECONDARY AND TERTIARY AMINES.
                                                                                                                                                       OZOLS J.; "Multiple forms of liver microsomal flavin-containing monooxygenases: complete covalent structure of form 2."; ARCH. BIOCHEM. BIOPHYS. 290:103-115(1991).
"Cloning and sequencing of flavin-containing monooxygenases FMO3 and FMO4 from rabbit and characterization of FMO3.";
J. BIOL. CHEM. 269:14314-14322(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM; PF00743; FMO-11ke; 1.
OXIDOREDUCTASE; MONOOXYGENASE; NADP; FLAVOPROTEIN; FAD; MICROSOME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: N.N-DIMETHYLANILINE + NADPH + O(2) = N.N-DIMETHYLANILINE N-OXIDE + NADP(+) + H(2)O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FAD (ADP PART) (POTENTIAL).

NADP (POTENTIAL).

M -> W.

M -> V.

D -> P (IN REF. 2).

STE -> ATC (IN REF. 2).

STE -> RO (IN REF. 2).

C -> E (IN REF. 2).

F -> FKDF (IN REF. 2).

W -> T (IN REF. 2).

S -> W (IN REF. 2).

W +> T (IN REF. 2).

W +> EW (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 530;
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1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36; DB 1;
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(REL. 35, LAST SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: MICROSOMAL.
-!- TISSUE SPECIFICITY: LIVER.
-!- SIMILARITY: BELONGS TO THE FWO FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MULTIGENE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COFACTOR: FAD FLAVOPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59684 MW;
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195
278
404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                 TISSUE=LIVER;
MEDLINE; 89374273.
                                                                                                                                 MEDLINE; 91378577.
                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82 HNSKLQ 87
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1 HSSKLQ 6
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DRP2_HUMAN
Q13474;
01-NOV-1997 (
01-NOV-1997 (
                                                                                                                                                                                                                                                                                                                                                                    OZOLS J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NP_BIND
NP_BIND
VARIANT
VARIANT
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                   BROWN D., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WOOD V.;
SUBMITED (SEP-1997) TO EMBL/GENBANK/ODBJ DATA BANKS.
-!- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + TRNA = S-ADENOSYL-L-HOMOCKSTEINE + TRNA CONTAINING S-METHYLAMINOMETHYL-2-
                                                                                                                                                      PROBABLE TRNA (5-METHYLAMINOMETHYL-2-THIOURIDYLATE)-METHYLTRANSFERASE (EC 2.1.1.61).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=ATCC 33530 / G-37;

MEDLINE, 96026346.

FRASER C.M., GOCANNE J.D., WHITE O., ADAMS M.D., CLAYTON R.A.,

FLEISCHMANN R.D., BULT C.J., KERLAYAGE A.R., SUTTON G., KELLEY J.M.,

FRITCHMAN J.L., WEIDMAN J.F., SMALL K.V., SANDUSKY M., FUHRMANN J.L.,

MGUYEN D.T., UTTERBACK T.R., SANDEK D.M., PHILLIPS C.A., MERRICK J.M.,

TOMB J.-F., DOUGHERTY B.A., BOTT K.F., HU P.-C., LUCIER T.S.,

PETERSON S.N., SMITH H.O., HUTCHISON C.A. III, VENTER J.C.;

SCIENCE 270:397-403(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MYCOPLASMA GENITALIUM.
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; MOLLICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 34; DB 1; Length 415; Pred. No. 1.58e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
HYPOTHETICAL ABC TRANSPORTER AIP-BINDING PROTEIN MG187.
                                                                                                                                                                                                                 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES;
SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, 298977; E339919; --
FRANSFERASE; TRNA PROCESSING.
TRANSFERASE; MFTHYLTRANSFERASE; TRNA PROCESSING.
                                                                                                            LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            585 AA.
                                                 415 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE TRMU FAMILY
                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                          CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MYCOPLASMATACEAE; MYCOPLASMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87.2%;
Similarity 66.7%;
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                               STANDARD;
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                                                                                                                                                                                                                                                                                     SCHIZOSACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                            15-JUL-1998 (REL.
15-JUL-1998 (REL.
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                   15-JUL-1998 (REL.
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1 HSSKLQ 6
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Y187_MYCGE
P47433;
                                               TRMU_SCHPO
                                                                                                                                                                                                 SPAC23H4.04
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                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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VINOGRADOV S.N., WALZ D.A.;
"The cDNA sequences encoding two components of the polymeric fraction of the intracellular hemoglobin of Glycera dibranchiata.";
J. BIOL. CHEM. 265:21843-21851(1990).
-: SUBUNIT: POLYMER.
-: THIS PROTEIN IS ONE OF AT LEAST SIX COMPONENTS IN THE POLYMERIC FRACTION OF GLYCERA HEMOGLOBIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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GLOBIN, POLYMERIC COMPONENT P2.
GLYCERA DIBRANCHIATA (BLOODWORM).
EUKARYOTA: METAZOA; ANNELIDA; POLYCHAETA; PHYLLODOCIDA; GLYCERIDAE;
FUNCTION: REQUIRED FOR NUCLEAR DIVISION. COULD FUNCTION IN THE
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Pred. No. 7.83e+00;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                               D3B877CC CRC32;
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PIR; A36529; A36529.
PROSITE; PC01033; GLOBIN; 1.
PFAM; PF00042; Globin; 1.
HSSP; P02216; 1HBG.
HEME; OXYGEN TRANSPORT; RESPIRATORY PROTEIN.
                                        -!- SUBCELLULAR LOCATION: NUCLEAR.
-!- SIMILARITY: TO YEAST ESP1 AND S.POMBE CUT1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (REL. 18, CREATED)
(REL. 18, LAST SEQUENCE UPDATE)
(REL. 36, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                          89.78;
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Similarity 66.7%;
4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                    PIR; A42854; A42854.
                        MITOTIC SPINDLE
                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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Matches 4; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1665 HAAKLQ 1670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 HNAKLQ 62
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1 HSSKLQ 6
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GLP2_GLYDI
P21659;
01-MAY-1991 (
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15-JUL-1998
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Gaps

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0; Indels

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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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GENETICS 129:1111-1117(1991).
-!- FOWTION: INVOLVED IN SEGMENT POLARITY. IS REQUIRED FOR THE NORMAL DEVELOPMENT OF THE POSTERIOR HALF OF EACH EMBRYONIC SEGMENT.
-!- SUBCELLULAR LOCATION: UNCLEAR.
-!- DEVELOPMENTAL STAGE: EXPRESSED UNIFORMLY THROUGHOUT THE BLASTODERM STAGE AND GASTRULATION AND DOES NOT RESOLVE INTO SEGMENTALLY REPEATING STRIPES UNTIL THE END OF THE SHORT PHASE OF GERM-BAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BERRY A.J., AJIOKA J.W., KREITMAN M.; "Lack of polymorphism on the Drosophila fourth chromosome resulting
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORENIC T.V., SLUSARSKI D.C., KROLL K.L., HOLMGREN R.A.;
Cloning and characterization of the segment polarity gene cubitus
interruptus Dominant of Drosophila.";
GENES DEV. 4:1053-1067(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTENSION. SIMILARITY: TO THE GLI-RELATED GROUP OF C2H2-TYPE ZINC-FINGERS
                                                                                                                                                                                                         .;
0
                                                                                                                                                                                                                                                                                                                                                                                                  DROSOPHILA MELANOGASTER (FRUIT FLY).
EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
                                                                                                                                                                                 Length 585;
                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                Score 34; DB 1; L
Pred. No. 1.58e+01;
                                                                                                                                          40 47 ATP (POTENTIAL).
585 AA; 66949 MW; EC78C4B8 CRC32;
                                                                                                                                                                                                                                                                                                                                    01-NOV-1990 (REL. 16, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-ETB-1996 (REL. 33, LAST ANNOTATION UPDATE)
CUBITUS INTERRUPTUS DOMINANT PROTEIN.
                                                                                                  PROSITE; PS00211; ABC_TRANSPORTER; 1.
PFAM; PF00005; ABC_tran; 1.
HYPOTHETICAL PROTEIN; ATP-BINDING; TRANSPORT.
                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                 87.2%;
66.7%;
                                                                             EMBL; U39696; G1045872; -.
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                                                                                                                                                                                                         Conservative
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PIR, S12769, S12769.
FLYBASE, FBGN0004859; ci.
                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                                 Query Match
Best Local Similarity
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MEDLINE; 92146935.
                                                                                                                                                                                                                                 226 HNAKLQ 231
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                                                                                          TIGR; MG187
                                                                                                                                                                                                                                                                                               LT 13
CID_DROME
P19538;
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SEQUENCE
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PROSITE; PS00028; ZINC_FINGER_C2H2; 4.

PFAM; PF00096; Zf-C2H2; 5.

HSSP; P08151; ZGLI.

BCSPCLOPMENTAL PROTEIN; SEGMENTATION POLARITY PROTEIN; ZINC-FINGER; METAL-BINDING; REPEAT; NUCLEAR PROTEIN.

DOMAIN 451 603 ZINC-FINGERS.
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0
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0
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 34; DB 1; Length 1524;
Pred. No. 1.58e+01;
0; Mismatches 1; Indels
                                                                                                                                                                                       Length 1377;
                                                                                                                                                                                                                0; Indels
                                                                                  C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
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W; E074D413 CRC32;
                                                                                                                                                                                    Score 34; DB 1; Le
Pred. No. 1.58e+01;
                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                  Mismatches
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HYPOTHETICAL PROTEIN KIAA0133
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llarity 83.3%;
Conservative
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66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE=BONE MARROW;
                                                                                                                                                                                                    Local Similarity
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1462
1524
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292
533
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996
993
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| HSSKLQ 6
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Q14146;
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ZN_FING
ZN_FING
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ZN_FING
ZN_FING
SN_FING
SEQUENCE
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1 HSSKLQ 6

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COLLED COLL (POTENTIAL).
TAIL.
ATP (POTENTIAL).
ACTIN-BINDING.
L -> F (IN REF. 2).
A -> T (IN REF. 2).
A -> T (IN REF. 2).
NKSGCFEIEGVSDEH -> IEWMFELKVYRWKS (IN REF. 2).
NKSGCFIIGVSDEH -> IEWMFELKYRWKS (IN REF. 2).
N -> K (IN REF. 2).
HH -> QQ (IN REF. 2).
HH -> QQ (IN REF. 2).
HH -> QQ (IN REF. 2).
                                                                                                                                                                                                                                                                                             [3]
SEQUENCE OF 182-298 FROM N.A.
MEDLINE; 95023928.
TITUS M.A., KUSPA A., LOOMIS W.F.;
"Discovery of myosin genes by physical mapping in Dictyostelium.";
PROC. NATL. ACAD. SCI. U.S.A. 91:9446-9450(1994).
-!- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO ACTIN AND HAS ATPASE
ACTIVITY THAT IS ACTIVATED BY ACTIN.
-: SUBUNIT: HOMODIMER (POTENTIAL).
-: SIMILARITY: BELONGS TO CLASS-5 MYOSINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P08799; IMND.
MYOSIN; REPEAT; ATP-BINDING; CALMODULIN-BINDING; ACTIN-BINDING;
HEPTAD REPEAT PATTERN; COILED COIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 34; DB 1; Length 2245;
Pred. No. 1.58e+01;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                    [2]
SEQUENCE OF 1-1021 FROM N.A.
PETERSON M.D., TITUS M.A.;
SUBMITTED (JAN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                     STRAIN-AX3;
HAMMER J.A. III, JUNG G.;
SUBMITTED (JAN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                   01-001-1996 (REL. 34, CREATED)
01-00T-1996 (REL. 34, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
                                                                                                                           DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
EUKARYOTA; DICTYOSTELIIDA; DICTYOSTELIUM.
                            PRT;
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258478 MW;
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EMBL; L35322; G1039361; -.
DICTYDB; DDD1095; MYOJ.
PFAM: PF00063; myosin_head; 2.
PFAM: PF00612; IQ; 3.
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Best Local Similarity 83.3%;
Matches 5; Conservative
                            STANDARD;
                                                                                                   MYOSIN IJ HEAVY CHAIN.
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2245 AA;
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Search completed: Thu Oct 28 11:20:45 1999 Job time: 8 secs.

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01-JAN-1998 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
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CYTB.
TOMOCICHLA TUBA.
MITOCHONDRION.
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                                                                                                                                                                                                                                                                                                                                                                            1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_lnvertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus
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CYTOCHROME B. 4
CYTOCHROME B. 4
RNA HELLCARE. 4
F6N15.5 PROTEIN. 8
ROYAL JELLY PROTEIN BG
GUANYLATE KINASE ASSOC BG
DAP-1 BETA. 8
PSD-95 BINDING PROTEIN B
                                                                                                                      Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd
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CORKSCREW PROTEIN (EC
HYPOTHETICAL 95.5 KD P
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SIMILARITY TO HUMAN PR
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Listing first 45 summaries
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(1-6) from US09081707.pep
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LAST SEQUENCE UPDATE)
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SUBMITTED (MAY-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
  01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
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Local Similarity 83.3%;
es 5; Conservative
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01-NOV-1998 (TREMBLREL.
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01-NOV-1998 (TREMBLREL.
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STRAIN-CV. COLUMBIA;
WATERSTON R.;
                                                                                                                                                                                                                                                                                                                                                     883 AA;
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EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII; TELEOSTEI; EUTELEOSTEI; ACANTHOPTERYGII; PERCOMORPHA; PERCIFORMES; LABROIDEI; CICHLIDAE; TOMOCICHLA.
                                                                                                                                                                                                                                                                                                                                                                                                                EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI; EUTELEOSTEI; ACANTHOPTERYGII; PERCOMORPHA; PERCIFORMES;
LABROIDEI; CICHLIDAE; CAQUETAIA.
                                                                                                                                                             PFAM; PF00033; cytochrome_b_N; 1.
MITOCHONDRION; ELECTRON TRANSPORT; RESPIRATORY CHAIN; TRANSMEMBRANE;
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                                                                                                                                                                                                                                   Gaps
                                                                                 FERROCYTOCHROME C.
-!- COFACTOR: TWO HEME GROUPS
(B562 AND B566) WHICH ARE NOT COVALENTLY BOUND TO THE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -:- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY BOUND TO THE PROTEIN
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                                                                                                                                                                                                              Score 37; DB 8; Length 378; Pred. No. 4.33e+00;
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                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MARTIN A.B., BERNINGHAM E.;
SUBMITTED (JUN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYTIC ACTIVITY: QH(2) + 2 FERRICYTOCHROME C = Q
FERROCYTOCHROME C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                          0
                                                 MARTIN A.P., BERMINGHAM E.;
SUBMITTED (JUN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYTIC ACTIVITY: QH(2) + 2 FERRICYTOCHROME C =
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LAST SEQUENCE UPDATE)
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Pred. No. 4.33e+00;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42425 MW; E7F49DA3 CRC32;
                                                                                                                                                                                         378 AA; 42344 MW; 2E7A3348 CRC32;
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                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                     378 AA.
                                                                                                                           EMBL; AF009941; G2281563; -.
PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
PFAM; PF00032; cytochrome_b_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF009940; G2281561; -.
PROSITE: PS00192; CYTCOCHROME_B_HEME; 1.
PFAM: PF00032; CYTCOCHROME_D_C; 1.
PFAM: PF00033; CYTCOTROME_D_N; 1.
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larity 83.3%;
Conservative
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023511;
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01-JAN-1098 (TREMBLREL. 05,
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05,
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Best Local Similarity 83.3%;
Matches 5; Conservative
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01-JAN-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
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Matches 5; Conser
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MEDLINE; 99121113.

MEDLINE; 99121113.

MEDLINE; 99121113.

REGRAMA M., BANCROFT W., VAN STAVEREN M., STIEKENA W., DEAN C.,

BEYAN M., BANCROFT W., VAN STAVEREN M., STIEKENA W., DROST L.,

REDLER P., HUDSON S.A., PATEL K., MURPHY G., PIFFANELLI P., WEDLER H.,

REDLER P., WARBOTT R., WEITZENEGGER T., POHLT T.M., TERRYN N.,

A GIELEN J., VILLARROEL M., LAO N., KAVANAGH T., HEMPEL S., KOTTER P.,

A GIELEN M., JAMES M., LAO N., KAVANAGH T., HEMPEL S., KOTTER P.,

B SILVEY M., JAMES R., MONTFORT A., PONS A., PUICDOMENECH P., DOUKA A.,

VOUKELATOU E., MILIONI D., HATZOPOULOS P., PIRAVANDI E., OBERMAIER B.,

A HILBERT H., DUESTERHOFT A., MOORES T., JONES J.D.G., ENEVA T.,

RA BELSENY M., VOLCKARET G., MEWES H.W., KLOSTERMAN S.,

SCHUELLEN C., CIALIMATZIS N.;

"Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of

NATURE 391.485-488(1998).
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EUKARYOTA; VIRIDIPLANYAE; STREPOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUFHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUKARXOTA; VIRIDIPLANȚAE; STREPTOPHYTĂ; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
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Pred. No. 4.33e+00;
1; Mismatches 0; Indels
                                                                                                                                                                          SEQUENCE FROM N.A.
EU ARABIDOPSIS SEQUENCING PROJECT, ESSA;
SUBMITTED (JUN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BANKS.
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SUBMITTED (JUN-1998) TO EMBL/GENBANK/DDBJ DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; 297341; E327007; PROSITE; PS00690; DEAH APP_HELICASE; PFAM; PF00271; helicase_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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RYAN E., EDWARDS J., PAPE K.;
"The sequence of A. thaliana I
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DESCRIPTION OF TREMELREL. 06, CREATED)
01-JUN-1998 (TREMELREL. 06, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMELREL. 06, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMELREL. 08, LAST SEQUENCE UPDATE)
PSD-95 BINDING PROTEIN.
RATTUS NORVEGICUS (RAT).
RATTUS NORVEGICUS (RAT).
SCIUNGGNATHI; MURIDAE; MURINAE; RATTUS.
                                                                                                                                                                                                                               EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE; 97431353.
SATOH K., YARNAH H., SENDA T., KOHU K., NAKAMURA T., OKUMURA N.,
MATSUMINE A., KOBAYASHI S., TOYOSHIMA K., AKIYAMA T.;
"DAP-1, a novel protein that interacts with the guanylate kinase-like
domains of hDLG and PSD-95.";
GENES TO CELLS 2:415-424(1997).
EMBL; ABOOG276; DO24134;
SEQUENCE 675 AA; 75260 MW; IFFEZAC4 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                      "GKAP, a novel synaptic protein that interacts with the guanylate kinase-like domain of the PSD-95/SAP90 family of channel clustering
                                                                                                                                                                                                                                                                                                                                              KIM E., NAISBITT S., HSUEH Y.P., RAO A., ROTHSCHILD A., CRAIG A.M., SHENG M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 36; DB 11; Length 666; Pred. No. 8.73e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 675;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             666 AA; 74233 MW; B3E3BB93 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       675 AA.
                                                                                                                                                                                                                                                      SCIUROGNATHI; MURIDAE; MURINAE; RATTUS
       1.T 8 PRELIMINARY; PRT; P97841 P97841; 01-MAY-1997 (TREMBLREL. 03, LAST SEO 01-MAY-1997 (TREMBLREL. 08, LAST SEO 01-NOY-1998 (TREMBLREL. 08, LAST AND GUANYLATE KINASE ASSOCIATED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CREATED)
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J. CELL BIOL. 136:669-678(1997).
EMBL; U67987; G1857139; -.
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08,
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HOMO SAPIENS (HUMAN).
REMERKOTA; METAZOA; CHORDATA
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 Match 92.3%;
Local Similarity 83.3%;
Local Similarity 83.3%;
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Best Local Similarity 83.3%;
Matches 5; Conservative
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                                                                                                                                                                                                           RATTUS NORVEGICUS (RAT)
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                    MEDLINE; 97177144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104 HSPKLQ 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94 HSPKLQ 99
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DT 011
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE: 97177144.
KIM E., NAISBITT S., HSUEH Y.P., RAO A., ROTHSCHILD A., CRAIG A.M., SHENG M.;
"GKAP, a novel synaptic protein that interacts with the guanylate kinase-like domain of the PSD-95/SAP90 family of channel clustering
                                                                                                                                   Gaps
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01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1997 (TREMBLREL. 03, LAST ANNOTATION UPDATE)
ROYAL JELLY PROTEIN RJP57-1 PRECURSOR.
APIS MELLIFERA (HONEYBEE).
EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
PTERYGOTA; HYMENOPTERA; APOCRITA; ACULEATA; APIDEE; APIS.
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STRAIN-8 DAYS OLD NIRSE HONEY BEE; TISSUE-HEAD;
KIAUDINI J., HANES J., KULIFAJOVA J., ALBERT S., SIMUTH J.;
J. ALUCULTURAL RES. 33:105-111(1994).
EMBL; 226318; E213552;
                                                                                  Length 509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 36; DB 5; Length 544;
Pred. No. 8.73e+00;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36; DB 4; Length 627; Pred. No. 8.73e+00; 1; Mismatches 0; Indels
                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vi mai-1994 (TREMBLREL. 03, LAST SEÓUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
GRADY.
                                                                             Score 36; DB 10; Pred. No. 8.73e+00;
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J. CELL BIOL. 136:669-678(1997).
EMBL; UG7988; G1857137;
ernTENCE 627 AA; 70051 WW; C40A3CBB CRC32;
EMBL; AF069299; G3193321; -
SEQUENCE 509 AA; 58562 MW; 5A682DOD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL 1 . 16 POTENTIAL.
SEQUENCE 544 AA; 61662 MW; 767820E6 CRC32;
                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                              544 AA
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Best Local Similarity 83.3%;
Matches 5; Conservative
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imilarity 83.3%;
5; Conservative
                                                                             92.3%;
Similarity 83.3%;
5; Conservative
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Best Local Similarity
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Best Local Similarity
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|HSSKLQ 6
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| HSSKLQ 6
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P78335
P78335;
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01-MAY-1997 (TREMBLREL. 03, CREATED)
01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
PSD-95/SAP90-ASSOCIATED PROTEIN-1.
RATHUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCIUROGNATHI; MURIDAE; MURIDAE; RATHUS.
                                                                                                                                                                                                                                                                                                                                                                                  HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE; 97431353.

SATOH K., YANAI H., SENDA T., KOHU K., NAKAMURA T., OKUMURA N.,

MATSUMINE A., KOBAYASHI S., TOYOSHIMA K., AKIYAMA T.,

"DAP-1, a novel protein that interacts with the guanylate kinase-like
domains of hold and 825-95.";

GENES TO CELLS 2:415-424 (1997).

EMBL; ABO00277; D1024115; -.

SEQUENCE 977 AA; 108872 MW; FFF0A0A0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 8.73e+00;
....arrhes 0; Indels
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Pred. No. 8.73e+00;
1; Mismatches 0; Indels
  Indels
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ID 014990

AC 014490

DT 01-7AN-1998 (TREMBLREL. 05, CREATED)

DT 01-NO-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)

DT 01-NO-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)

DT 01-NO-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

DE DAP-1 ALCHA.

CS UKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUT

CATARRHINI: HOMINIDAE: HOMO.

RN SEQUENCE FROM N.A.

RX MEDLINE: 97431553.

RA MATSUNINE A., KORAYASHI S., TOYOSHIMA K., AKIYAMA T.;

RT "DAP-1, a novel protein that interacts with the quanyla domains of hDLG and PSD-95.";

RT GENES TO CELLS: 2415-44(1997).

DR EMBL: ABOROCZ77: D10244155; -..

SQ SEQUENCE 977 AA; 108872 MW; FFFORORO CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P91339
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TAKAI Y., TAKEUCHI M., IRIE M., HATA Y.;
J. BIOL. CHEM. 0:0-0(0).

SEQUENCE 992 AA; 110177 MW; 7D090FD0 CRC32;
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Local Similarity 83.3%;
les 5; Conservative
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Similarity 83.3%;
5; Conservative
  Conservative
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Best Local Similarity
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P97836
P97836;
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MEDLINE; 94378523.
FIEDLING P.A., LAMBDEN P.R., CAUL E.O., CLARKE I.N.;
FIEDLING P.A., LAMBDEN P.R., CAUL E.O., CLARKE I.N.;
"Molecular characterization of the outer capsid spike protein (VP4)
gene from human group C rotavirus.";
VIROLOGY 204:442-446(1994).
EMBL; X79441; G495229;
EMBL; X79441; G495229;
SEQUENCE 744 AA; 84036 MW; CDD47684 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE, 94378523.
FIELDING P.A., LAMBDEN P.R., CAUL E.O., CLARKE I.N.;
MODICULAR CHARCELIZATION Of the outer capsid spike protein (VP4)
gene from human group C rotavirus.";
VIROLOGY 204:442-445(1994).
BMBL, X79442, 6495231;
BMBL, X79442, 6495231;
SEQUENCE 744 AA: 84080 MW; 4E128877 CRC32;
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                                                                                                                                                                                                                                                                                                           Gaps
                                                   KAWASHIMA N., TAKAMIYA K., SUN J., KITABATAKE A., SOBUE K.;
"Differential expression of isoforms of PSD-95 binding protein (GRAPYSAPAP1) during rat brain development.";
FEBS LETT . 488 3301-304(1997).
EMBL; AB003594; D1025176; -.
SEQUENCE 692 AA; 76991 MW; CD061633 CRC32;
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                                                                                                                                                                                                                                         Score 36; DB 11; Length 692;
Pred. No. 8.73e+00;
1; Mismatches 0; Indels
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LAST ANNOTATION UPDATE)
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VIRUSES; DSRNA VIRUSES; REOVIRIDAE; ROTAVIRUS.
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VIRUSES; DSRNA VIRUSES; REOVIRIDAE; ROTAVIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 744 AA.
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Best Local Similarity 83.3%;
Matches 5; Conservative
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Best Local Similarity
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  SEQUENCE FROM N.A
                                  MEDLINE; 98089008
                                                                                                                                                                                                                                                                                                                                                           102 HSPKLQ 107
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| HSSKLQ 6
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LT 12 Q82040 Q82040;

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Matches

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RABDITINA: RHABDITIDAE; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.

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RE STAINAMENTATION N3.

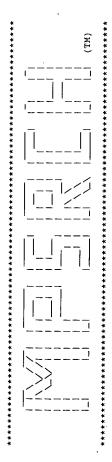
RA MILSON N. AINSCOUGH N. ANDERSON K., BAYNES C., BERKS M., CONDER J., COULSON A., FULLON L., ALNSCOUGH N., ALNSCOUGH N., ALNSCOUGH J., COOPER J., ENGRING R. A., RERGHAN J., RIGHTON L., ALSTER M., ALSTER M., ALSTEN M., LAISTER M., LAISTER M., LAISTER M., LAISTER M., COOPER J., LLOYD L., ALSTER M., COOPER J., LLOYD L., ALSTER M., ANDERSON J., ENGRAND R., RA MALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J., RA MATSON A., WEINSTOCK L., WILKINSON B., WATSON A., WEINSTOCK L., WILKINSON B., COOPER A., LE T., E T., E
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Search completed: Thu Oct 28 11:22:09 1999 Job time: 42 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Oct 28 11:24:16 1999; MasPar time 3.30 Seconds 45.117 Million cell updates/sec Run on:

Tabular output not generated

>US-09-081-707-10 (1-7) from US09081707.pep 45 Title: Description: Perfect Score:

1 EHSSKLQ 7 Sequence: PAM 150 Gap 15 Scoring table:

170751 seqs, 21266608 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

a-geneseq35 Database:

i:part1\_2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part12 13:part13 14:part14 15:part12 15:part12 15:part12 15:part13 16:part12 17:part17 18:part23 14:part24 25:part25 26:part26 27:part27 28:part28 29:part29 30:part30 31:part31 32:part32 33:part33 34:part34 35:part35 36:part36 37:part37 38:part38

Mean 13.622; Variance 31.430; scale 0.433 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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Result		Query					
No.	Score	Match	Match Length DB	DB,	ID	Description	Pred. No.
			1 0	: ;			
-	7 5	73.3	766	34	W69/42	SAPAP2 protein.	4.21e+01
7	42	93.3	992	34	W69740	SAPAP1 protein.	4.21e+01
m	38	84.4	210	35	W70284	Anaplasma marginale m	1.51e+02
4	38	84.4	462	26	W33420	Human semenogelin I.	1.51e+02
Ŋ	38	84.4	462	17	R89583	Human semenogelin I.	1.51e+02
9	36	80.0	432	36	W72182	HSV-2 strain SB5 Cont	2.80e+02
7	36	80.0	497	35	W72030		2.80e+02
ω	36	80.0	497	36	W72132	HSV-2 strain SB5 Cont	2.80e+02
σ	36	80.0	735	34	W69752	Herpes simplex virus-	2.80e+02
10	35	77.8	212	7	R08121	Modified tilapia prol	3.81e+02
11	35	77.8	212	7	R06893	Tilapia prolactin I.	3.81e+02
12	35	77.8	742	14	R74094	Human zona pellucida-	3.81e+02
13	35	77.8	2431	Ŋ	R25138	SFV4 non-structural p	3.81e+02
14	35	77.8	3084		W50891	Mouse laminin A chain	3.81e+02
15	34	75.6	7	24,	W27419	CDR2 from light chain	5.15e+02
16	34	75.6	118	18	R97559	Tomato pZ130 cDNA-enc	5.15e+02

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Gaps

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Score 42; DB 34; Length 992; Pred. No. 4.21e+01; 1; Mismatches 0; Indels

Query Match 93.3%; Best Local Similarity 85.7%; Matches 6; Conservative

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Tomato ovary-specific 5.15e+02 Humanised light chain 5.15e+02 Humanised light chain 5.15e+02 Humanised light chain 5.15e+02 Humanised light chain 5.15e+02 Ovary tissue transcri 5.15e+02 Ovary tissue transcri 5.15e+02 Muscae RNA-binding pro 5.15e+02 WD-40 domain-contg, h 5.15e+02 WD-40 domain-contg, h 5.15e+02 WD-40 domain-contg, h 5.15e+02 Maltose binding prote 5.15e+02 Maltose binding prote 5.15e+02 Invasin-maltose bindi 5.15e+02 Invasin-maltose bindi 5.15e+02 Maltose binding prote 5.15e+02 WHeat granule-bound s 5.15e+02 WHeat granule-bound s 5.15e+02 WHeat granule-bound s 5.15e+02 Streptokinass/maltose 5.15e+02 Streptokinass/maltose 5.15e+02 Modified streptokinas 5.15e+02	LIGNMENTS  2 AA.  1 protein; PSD-95/SAP90; diagnosis; interference; structural interference; structural interference; ekinase; neuronal disease.  2 JIGYODAN.  2 JIGYODAN.  3 JIGYODAN.  3 JIGYODAN.  4 In SAPAP 2 - useful for diagnosis and diseases and an annual protein having an amino acid an annual protein having an amino acid ane as SAPAP2; (B) a cDNA sequence encoding APAP2 or (C) an amino acid sequence encoding APAP2 or (C) an amino acid sequence hybridised tial sequence. SAPAP2 is a new animal fically with PSD-95/SAP90 and its related ediagnosis, prevention and treatment of sed by functional or structural interference
W08364 W21855 W21855 W21883 W21883 W38464 W38464 W38466 W31152 W38466 W41152 W43304 W61152 W61152 W61152 W61152 W61152 W61152 W61152 W61152 W61152 W611727 W21727 W21727 W21727 W21727 W21727	ALIGI al pi int int ko Ji ko Ji
022222	ry)  ry)  ry)  SHI  SHI  SHI  Shi  cop  ste
1127 1127 1127 1127 1127 1127 1127 1127	W69742 standard; protein; 9 W69742; 26-OCT-1998 (first entry) SAPAP2 protein. Human; SAPAP2; SAPAP1; anim nervous disease; functional membrane associated quanyla Homo sapiens. 104.201478-A. 104.201478-A. 104.201478-A. 104.201478-A. 104.201478-A. 104.301715, 24.7AN-1997; 011715, 24.7AN-1997; 011715, 34.7AN-1997; 011715, 34.7AN-1907; 011717, 011
0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.	W69742 standard; prote W69742 standard; protein W69742. W69742. W69742. W69742. W69742. W69742. SAPAP2 protein. Human; SAPAP2; SAPAP1. Human; SAPAP2; SAPAP1. Homo sapiens. U10201478-A. U4-UAN-1997; D1715. U4-UAN-1997; D1715. U4-UAN-1997; D1715. UAN-1997; D17171. UAN-1998. UAN-1997; D17171. UAN-1998. UAN-
.  ***********************************	W69742 standa W69742; 26-02T-1998 SAPAP2 protei Human; SAPAP2 nervous disea nembrane asso 10021478-A. 10021478-A. 10021478-A. 10021478-A. 10021478-A. 1001478-A. 1001478-A. 1001478-A. 1001478-A. 1001478-A. 1001478-A. 1001478-A. 1001478-A. 1001478-A. 100148-A. 1001478-A. 10014
LHII ZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZ	CO .
	NO CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC

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Purity No. 7 Mills 15. The control of Anaplasma species in rickettsemia - uses specific ELISA detection of Anaplasma species in rickettsemia - uses specific monoclonal antibodies against Anaplasma major surface protein 5 Disclosure; Columns 5-8; 7pp; English.

The present sequence represents the Anaplasma marginale major surface protein 5 (MSP-5). The invention provides a method for detecting anaplasmosis, a vector-borne rickettsial disease of cattle, sheep and goats. The method involves using the monoclonal antibody (mab) ANAF16C1 and the Anaplasma MSP-5 protein in a competitive inhibition-ELISA format for the serological detection of cattle, sheep or goats infected with A marginale. The test is specific for Anaplasma species as the MSP-5 protein detected is found in all Anaplasma species and the mab ANAF16C1 used to detect it is specifically raised against it. The detection method is claimed to be capable of accurately detecting the protein due to its specificity. Previous methods e.g. nucleic acid hybridisation, cannot always detect carriers because of cyclic changes in rickettsemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New protein SAPAPI - used for, e.g. diagnosis and prevention of various neuronal diseases claim 1; page 4-7; 12pp; Japanese.

Claim 1; page 4-7; 12pp; Japanese.

The present sequence represents the SAPAPI protein having a 992 amino acid (aa) sequence. Also described in the present invention are: (1) an animal protein having an as sequence substantially homologous to SAPAPI; (2) cDNA sequence encoding SAPAPI; or an as sequence substantially homologous to SAPAPI, and (3) a genomic DNA sequence hybridised to the CDNA or its partial sequence. SAPAPI is a novel animal protein specific for PSD-95/SAP90 and its related protein, and may be useful for the diagnosis, prevention and treatment of various neuronal diseases caused by functional or structural interference of nervous system.
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Anaplasma marginale major surface protein-5.
Anaplasma marginale major surface protein-5; MSP-5; anaplasmosis;
rickettsemia; cattle; sheep; goat; ELISA; monoclonal antibody ANAF16C1;
mAb; competitive inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                      SAPAPI protein.
Human; SAPAPI; SAPAP2; animal protein; PSD-95/SAP90; diagnosis;
nervous disease; functional interference; structural interference;
membrane associated guanylate kinase; neuronal disease.
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Pred. No. 4.21e+01;
1; Mismatches 0; Indels
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16-OCT-1996: 730995.
16-OCT-1996: US-730995.
16-OCT-1996: US-730995.
(UNIW ) UNIV WASHINGTON STATE RES FOUND.
(USDA ) US SEC OF AGRIC.
DAVIS WC, RIOWLES DP, McElwain TF, McGuire TC, Palmer GH;
                                                                                                                                                                                                                                                                                                                                                                                                24-JAN-1997; 011714.
24-JAN-1997; JP-011714.
(KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
(TAKE/) TAKEUCHI M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W70284 standard; Protein; 210 AA.
                                          W69740 standard; protein; 992 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.3%;
85.7%;
                                                                                                       26-OCT-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anaplasma marginale.
US5798219-A.
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Best Local Similarity
Matches 6; Conser
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distipled useful in assays lot active antigen, and in assays lot active antigen, and in assays lot active antigen, and in assays lot prostatic cancer treatment bisclosure; Fig 1, 192pp; English.

The present sequence represents Semenogelin I, a major sperm entrapping gel protein. Oligopeptides designed based on the sequences surrounding prostate specific antigen (PSA) cleavage sites (indicated above, and numbered in order of the relative affinity of a site towards PSA hydrolysis) are claimed. PSA, which has chymotrypsin-like specificity is responsible for dissolution of the gel structure formed at ejaculation by proteolysis of the major gel proteins (Semenogelin I and II, and fibronectin). Liquefaction of the ejaculate releases progressively motile spermatozoa. PSA complexed to alpha l-antichymotrypsin is the predominant form of serum PSA. Serum measurements of PSA are useful for monitorinom of the prostate. Prostate metastases are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             also known to secrete immunologically reactive PSA since serum PSA is detectable at high levels in prostatectomised patients showing widespread metastatic prostate cancer. Cytotoxic compounds that could be activated by the proteolytic activity of PSA should also be prostate cell specific as well as specific for PSA secreting prostate metastases. Conjugates of prostate cancer. The oligopeptides are useful in treatment of prostate cancer. The oligopeptides can also be used in a quantitative assay for enzymatically active PSA.
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                                     Gaps
                                                                                                                                                                                                                                                       Oligopeptide; proteolytic cleavage; prostate specific antigen; PSA; cleavage site; Semenogelin I; chymotrypsin-like; serum RSA; human; adenocarcinoms; prostate metastases; prostate cancer; treatment; detection; cytotoxic conjugate; activation; quantitative assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI: 97-225974/20.
Oligopeptide(s) recognised and cleaved by free prostate specific
antigen - useful in assays for active antigen, and in
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 Length 210;
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Pred. No. 1.51e+02;
1; Mismatches 0; Indels
Score 38; DB 35; Length 210
Pred. No. 1.51e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MERI ) MERCK & CO INC.
DeFeo-Jones D, Feng D, Garsky VM, Jones RE, Oliff AI;
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+-= "Cleavage site
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376..377
' -+^= "Cleavage site
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289..290
. -+a= "Cleavage site
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j..350
..- "Cleavage s
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W33420 standard; Protein; 462 AA.
W33420;
 84.4%;
llarity 57.1%;
Conservative
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                                                                                                                                                                                                                 27-MAR-1998 (first entry)
Human semenogelin I.
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02-OCT-1996; U15713.
06-OCT-1995; US-540412.
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 Query Match
Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
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1 EHSSKLQ 7
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FHSSKLQ

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101 dhtakle 107
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1 EHSSKLQ 7
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1 EHSSKLQ 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New peptide substrates cleaved by prostate-specific antigen - also cytotoxic conjugates for traating prostate cancer, and assay for determination of PSA activity.

Tytotoxic conjugates for treating prostate cancer, and assay for determination of PSA activity.

Example 1: Pages 50-51: 142pp; English.

The present sequence is human semenogelin I (hSI), one of the major proteins, including hSII and fibronectlin, in the sperim entrapping gel formed at ejaculation. This gel structure undergoes dissolution proteins of prostate specific antigen (PSA), a protease with chymotrypsin like specificity, which proteolyses the above major proteins. New peptide substrates cleaved by PSA, i.e. peptides contg. a hSI PSA cleavage site, can be used in assays to determine the proteolytic activity of free PSA in a sample, and to identify cpds. which inhibit the proteolytic activity of free PSA in a sample, and to identify cpds. which inhibit the proteolytic activity of PSA, they may also be conjugated, via a covalent bond or peptide linker, to a cytotoxic agent and used to treat prostate cancer. In a PSA hydrolysis assay, the percentage of hSI cleaved by YORK PSA after
                                                                                                                  Human: semenogelin I; sperm entrapping gel; ejaculation; protease; gel structure; dissolution; prostate specific antigen; proteolysis; chymotrypsin like specificity; peptide substrate; cleavage site; assay; determination; proteolytic activity; identification; inhibitor; cytotoxic agent; conjugated; treatment; prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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HSV-2 strain SB5 Contig ID 15 ORF#15 protein.
HSV-2 strain SB5; immunological response induction; therapy; antiviral identification; viral protein inhibitor.
WO9820016-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 38; DB 17; Length 462;
Pred. No. 1.51e+02;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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R89583 standard; protein; 462 AA
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imilarity 85.7%;
6; Conservative
                                                            (first entry)
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28-JUN-1994; US-267092.
15-MAR-1995; US-404833.
(MBR.) MERCK & CO INC.
DeFeo-Jones D, Feng D, C
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31-OCT-1997; U20016.
                                                                                              Human semenogelin I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DeFeo-Jones D, Fer
WPI; 96-077275/08.
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                                                         02-SEP-1996
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This sequence represents a Herpes simplex virus type-2 (HSV-2) protein sequence of the invention. This sequence was isolated from a HSV-2 strain sequence of the invention. This sequence was isolated from a HSV-2 strain SB5 (deposited as ATCC VR-2546) DNA fragment designated Contig ID 15. Dased on homology, this sequence is a probable DNA packaging protein. The proteins can be used for the treatment or prevention of disease, to induce an immunological response in a mammal or to identify inhibitors, activators or novel antivirals. Antagonists of the proteins can be used to onhibit a viral polypeptide. The DNA sequence or a vector containing it can also be used to induce an immunological response in a mammal.
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                                                                                                                                                                                                    Herpes simplex virus type-2 sequences - useful in, e.g. preventic and treatment of infection or inducing immunological response in
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HSV-2 strain SB5; immunological response induction; therapy; antiviral identification; viral protein inhibitor.
Herpes simplex virus type 2.
W098201016-A1.
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Pred. No. 2.80e+02;
............... 0; Indels
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                                                                 Chan JY, Dabrowski-Amaral CE, Delvecchio AM, Dillon SB,
Esser KM, Leary JJ:
WPI; 98-286847/25
N-PSDB; V62176.
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Esser KM, Leary JJ:
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31-OCT-1997; U20016.
09-JUN-1997; US-049018.
04-NOV-1996; US-030279.
(SMIK ) SMITHKLINE BEECHAM CORP.
04-NOV-1996; US-030279.
(SMIK ) SMITHKLINE BEECHAM CORP.
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Best Local Similarity 42.9%;
Matches 3; Conservative
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WPI; 98-286847/25.
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                                                                                                     Sequence
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**Treening assays for antiviral agents - based on inhibition of herpes simplex UL15 and vP5 interaction or function

**Streening assays for antiviral agents - based on inhibition of herpes simplex viruse;

**Rethods have been developed for: (1) identifying an antiviral agent useful in treating infection with herpes viruse, comprising: (a) providing UL15 of herpes simplex virus-1 (HSV-1) or a functional cor homologue to come into association with a test compound; (c) providing VP5 of HSV-1 or a functional derivative or homologue thereof; (d) screening for inhibition of the interaction between UL15 or its convention for inhibition of the interaction between UL15 or its convention of the interaction between UL15 or its convention to homologue and VP5 or its derivative or homologue, where such inhibition is indicative that the test compound is an antiviral agent; (2) identifying an antiviral agent useful in treating infection with herpes viruses, comprising: (a) providing VP5 of herpes simplex virus-1 (HSV-1) or a functional conventive or homologue thereof; (b) permitting VP5 or its derivative
                                                                                                                                                                                                                                                                                                                            This sequence represents a Herress simplex virus type-2 (HSV-2) protein sequence of the invention. This sequence was isolated from a HSV-2 strain SEG (deposited as ATCC VR-2546) DNA fragment designated Contig ID 16. Based on homology, this sequence is a probable DNA packaging protein. The proteins can be used for the treatment or prevention of disease, to induce an immunological response in a mammal or to identify inhibitors, activators or novel antivirals. Antagonists of the proteins can be used to induce an immunological response in a mammal. Sequence or a vector containing it can also be used to induce an immunological response in a mammal.
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Herpes simplex virus type-2 sequences - useful in, e.g. prevention and treatment of infection or inducing immunological response in
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Herpes simplex virus-1 UL15 protein.
Herpes simplex virus-1; HSV-1; UL15; VP5; UL19; antiviral agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                            23-DEC-1998 (first entry)
HSV-2 strain SB5 Contig ID 16 ORF#8 protein.
HSV-2 strain SB5; immunological response induction; therapy; antiviral identification; viral protein inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36; DB 36; Length 497; Pred. No. 2.80e+02;
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                                                                                                                                                                                                       chan JÝ, Dabrowski-Amaral CE, Delvecchio AM, Dillon SB, Esser KM, Leary JJ; WPI; 98-286847/25.
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                                                                                                                                                                                                                                                                                                                      Claim 10; Page 95; 748pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JT 9
W69752 standard; protein; 735 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-FEB-1998; 301123.
21-FEB-1997; US-038914.
(SMIK ) SMITHKLINE BEECHAM CORP.
   T 8
W72132 standard; Protein; 497 AA.
                                                                                                                                                                                              (SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Herpes simplex virus type 1.
EP-860700-A2.
                                                                                                        Herpes simplex virus type 2. WO9820016-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Conservative
                                                                                                                                                   31-OCT-1997; U20016.
09-JUN-1997; US-049018.
04-NOV-1996; US-030279.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             166 dhtakle 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                identification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-AUG-1998.
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                                                                                                                                                                                                                                                                                                           mamma]
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Claim 10; Fig 2bis; 29pp; English.

The sequence was deduced from a cDNA clone isolated from a library preparation of the anterior plutiery gland of rilapia. It encodes a modified prolactin (TPRLI) which is thought to play an important role in osmoregulation (Hydromineral balance) in this species. The gene can be expressed using the strong promoter of gene 10 of bacteriophage T?. The gene was modified to remove the signal peptide coding region and the vector expressed in E.coli HB101. The protein differs from R06893 at only two positions: Leu and Ser replace Phe and Thr at AAs 7 and 100 resp.

The product can be admin. to culturing conditions. Dosage is 5 improve their adaptation to culturing conditions. Dosage is 5 in grid food/day. R06914 and R08122.

See also R06893, R06914 and R08122.
or homologue to come into association with a test compound; (c) providing UL15 of HSV-1 or a functional derivative or homologue thereof; (d) screening for inhibition of the interaction between the VP5 or its derivative or homologue and UL15 or its derivative or homologue, where such inhibition is indicative that the test compound is an antiviral agent. The present sequence represents the HSV-1 UL15
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                                                                                                                                                                                                                                                                                                Gaps
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Modified tilapia prolactin I.
Fish; hydromineral balance; pituitary; hormone; osmoregulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New recombinant fish polypeptide(s) - having growth and/or osmoregulatory properties for enhancing growth and adaption of
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                                                                                                                                                                                                                                             Length 735;
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Pred. No. 3.81e+02;
2; Mismatches 1
                                                                                                                                                                                                                                                Score 36; DB 34; I
Pred. No. 2.80e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="calculated as 20.9 kD"
                                                                                                                                                                                                                                                                                                   4; Mismatches
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/label=signal peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RentierDelrue F, Martial J, Renard WPI; 90-283784/38.
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R06893 standard; protein; 212 AA.
806893;
22-JAN-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T 10
R08121 standard; protein; 212 AA.
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/label=TPRLI
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larity 57.1%;
Conservative
                                                                                                                                                                                                                                                Query Match
Best Local Similarity 42.9%;
                                                                                                                                                                                                                                                                                                   3; Conservative
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06-JAN-1989; EP-400047.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oreochromis niloticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                              735 AA;
                                                                                                                                                                                                                                                                                                                                                           101 dhtakle 107
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1 EHSSKLQ 7
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                                                                      2 HSSKLQ 7
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                                                                                                                                                                                                               -JAN-1993
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The human zona pellucida-2 (HZP-2) protein may be used as a vaccine antigen. It can be artificially synthesised using recombinant techniques. Partial sequences of the HZP-2 gene were subcloned, the sequences and primers used in cloning and subcloning are given in 092255-69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence was deduced from a cDNA clone isolated from a library prepd. from mRNA extracted from the anterior pituitary gland of tilapia. It encodes a prolactin (PRLI) which is thought to play an important role in osmoregulation (hydromineral balance) in this species. The gene can be expressed using the strong promoter of gene 10 of bacteriophage T7. The gene was modified to remove the signal peptide coding region and the vector expressed in E.coli HB101. The product can be admin. to fish cultures to enhance growth and improve their adaptation to culturing conditions. Dosage is 5 ng-1 ug protein/g fish/day by injection or 1 ug-1 mg protein/g fish food/day.
Tilapia prolactin I.
Fish; hydromineral balance; pituitary; hormone; osmoregulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coding human zona pellucida-2 protein - used as a vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                New recombinant fish polypeptide(s) - having growth and/or osmoregulatory properties for enhancing growth and adaption of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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Pred. No. 3.81e+02;
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Pred. No. 3.81e+02;
2; Mismatches 0; Indels
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04-JAN-1996 (first entry)
Human zona pellucida-2 (HZP-2) protein.
Human zona pellucida; HZP-2; protein; vaccine; antigen;
                                                                                                                                                                                                             /note="calculated as 20.9 kD"
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                                                                                                                   1..24
/label=signal peptide
                                                                                                                                                                                                                                                                                                                                                  RentierDelrue F, Martial J, Renard A;
                                                                 niloticus.
Location/Qualifiers
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R74094 standard; Protein; 742 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 10; Fig 2; 29pp; English.
                                                                                                                                                            25..212
/label=TPRLI
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ilarity 66.7%;
Conservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77.8%;
57.1%;
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05-OCT-1993; 249404.
05-OCT-1993; JP-249404.
(TOU) TONEN CORP.
WPI: 95-182067/24.
N-PSDB; 092254.
                                                                                                                                                                                                                                                      19-SEP-1990.
06-JAN-1989; 400047.
06-JAN-1989; EP-400047.
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Best Local Similarity
Matches 4; Conserv
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N-PSDB; Q05981.
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1 EHSSKLQ 7
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J07099974-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fish cultures
                                                                   Oreochromis
                                                                                                                                                                                                                                   EP-387457-A
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Matches
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Gaps

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RNA mol. derived from alphavirus RNA genome - chimeric alphavirus antigen and vaccine for immunisation against viral infections Disclosure; Fig 5; 94pp; English.

The sequence given is the non-structural polyprotein encoded by a full length Semilki forest virus (SFV) cDNA clone within an SP6 expression vector. The SP6 RNA polymerase promoter allows in vitro transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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This is the amino acid sequence of the mouse laminin A chain. The primary object of the invention is to use laminin, laminin-derived protein fragments and/or laminin-derived polypeptides as potent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse laminin A chain.

Down's syndrome; hereditary cerebral haemorrhage; inflammation; malignancy; Familial Mediterranean Fever; multiple myeloma; malignancy; Familial Mediterranean Fever; multiple myeloma; Gertstmann-Straussler syndrome; kuru; scrapie; haemodialysis; carpal tunnel syndrome; senile cardiac amyloid polyneuropathy; Familial Amyloidotic Polyneuropathy; thyroid carcinoma; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Castillo G, Snow AD;
WHI 98-240534/J1.
Use of laminin and fragments - for developing products for use in
the diagnosis and treatment of amyloid disease, e.g. Alzheimer's
                                                                                    SFV4 non-structural polyprotein.
Semliki forest virus; SFV; SP6 expression vector; RNA polymerase.
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/note= "fourth globular domain repeat (Claim 13)"
2690..2700
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                                                                                                                                                                                                                                                                                                                                                                                                                                          vector. The SP6 RNA polymerase promoter a of full length and infectious transcripts.
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T 13
R25138 standard; Protein; 2431 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 77.8%;
Local Similarity 57.1%;
les 4; Conservative
                                                                 (first entry)
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08-OCT-1997; U18145.
08-OCT-1996; US-027981.
(UNIW ) UNIV WASHINGTON.
                                                                                                                                                                                                                                     (BIOP-) BIOPTION AB.
Garoff H, Liljestrom P;
WPI; 92-234633/28.
N-PSDB; Q26021.
                                                                                                                                                                        25-JUN-1992.
12-DEC-1991; SE0855.
13-DEC-1990; SE-003978.
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inhibitors of amyloid formation, deposition, accumulation and/or persistence in Alzheimer's disease and other amyloidoses. The camainin products (see W50888-98) may include mouse or human laminin A or Al Chain, laminin Blot B2 chain, laminin A2 chain (merosin). C laminin G1 chain, the globular repeats of the laminin A1 chain and the brea-amyloid binding domain of the laminin A chain. A claimed method for treating an amyloid disease comprises administering a polypeptide having a conformational similarity to a fragment of a polypeptide having a conformational similarity to a fragment of a minolyves determining levels of laminin in a sample. Production of laminin or its fourth globular repeat in vivo provides a method for involves determining levels of laminin in the products. The products and methods can be used for the diagnosis, prognosis, monitoring cand treatment of amyloidoses such as Alzheimer's disease. Down's syndrome and hereditary cerebral hemocranage with amyloidosis of the butch type (where the specific amyloid is the beta-amyloid protein), the amyloidosis associated with chronic inflammation.

Syndrome forms of malignancy and familial Mediterranean Fever (AA amyloid or inflammation-association and other B-cromailities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nakamura K, Takatsu K;
WPI: 97-202249/18.
Antibody against alpha-chain of human interleukin 5 receptor -
useful for diagnosis and treatment of respiratory allergic diseases,
e.g. chronic bronchitis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AL amyloid), the amyloidosis associated with type II diabetes (amylin or islet amyloid), the amyloidosis associated with prion diseases including Creutzfeldid-Jacob disease, Gertstmann-Straussler syndrome, kuru and animal scrapie (PrP amyloid), the amyloidosis associated with long-term haemodialysis and carpal tunnel syndrome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (beta 2-microglobulin amyloid), the amyloidosis associated with senile cardiac amyloid and Familial Amyloidotic Polymeuropathy (prealbumin or transthyretin amyloid), and the amyloidosis associated with endocrine tumours such as medullary carcinoma of
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W27419 standard; peptide; 7 AA.
W27419;
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11-SEP-1995; JP-232384.
(KYOW ) KYOWA HAKKO KOGYO KK.
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71.48;
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nes 5; Conservative
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Oct 28 11:24:52 1999; MasPar time 2.96 Seconds 94.825 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-081-707-10 (1-7) from US09081707.pep 45 Description: Perfect Score:

1 EHSSKLQ 7 Sequence:

Scoring table:

122810 seqs, 40068593 residues PAM 150 Gap 15 Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Mean 18.827; Variance 17.198; scale 1.095 pir60 1:pir1 2:pir2 3:pir3 4:pir4 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

		æ					
Result		Query					
No.	Score	Match	Match Length DB	DB	ID	Description	Pred. No.
7	45	100.0	582	7	A43412	semenogelin II precur	1.66e-01
8	42	93.3	509	7	T01344	hypothetical protein	1.20e+00
ĸ	42	93.3	675	m	T00013	DAP-1 beta protein -	1.20e+00
4	42	93.3	692	7	T00025	PSD-95 binding protei	1.20e+00
ស	42	93.3	977	က	T00014	DAP-1 alpha protein -	1.20e+00
9	40	88.9	265	7	S63532	NAD(P)H-quinone oxido	4.25e+00
7	40	88.9	585	7	G64220	ATP-binding protein m	4.25e+00
<b>6</b> 0	39	86.7	147	7	S13157	hemoglobin - polychae	7.87e+00
σ	39	86.7	585	7	E64892	probable membrane pro	7.87e+00
10	38	84.4	210	~	A49213	major surface protein	1.44e+01
11	38	84.4	224	~	G71281	probable Mq2+ transpo	1.44e+01
12	38	84.4	337	7	B44478		1.44e+01
13	38	84.4	373	Ŕ	A44478	probable cell growth	1.44e + 01
14	38	84.4	420	7	A54759	cytochrome ba(3) chai	1.44e+01
15	38	84.4	462	Н	WTHUB	semenogelin I precurs	1.44e+01
16	38	84.4	256	7	T03114	tegument protein - al	1.44e+01
17	38	84.4	617	7	T02121	hypothetical protein	1.44e+01
18	38	84.4	664	~	S58162	hypothetical protein	1.44e+01
19	37	82.2	91	7	E65011	hypothetical protein	2.61e+01
20	37	82.2	278	7	H65069	hypothetical protein	2.61e+01
21	37	82.2	356	-	S55437	translation releasing	2.61e+01
22	37	82.2	604	7	866993	hypothetical protein	2.61e+01
23	37	82.2	700	7	A61527	stonustoxin beta chai	2.61e+01

S29155 Schneider, K.; Kausler, W.; Tripier, D.; Jouvenal, K.; Spitchler, G. Biol. Chem. Hoppe-Seyler (1989) 370:353-356 Isolation and structure determination of two peptides

#journal #title #authors

##molecule\_type mnA ##residues 3-582 ##label LI2 ##cross-references GB:M81652 REFERENCE \$29155

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##molecule_type mRNA
                                    Query Match
Best Local Similarity
Matches 6; Conser
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                                                                                                        simultaneously with the sequence with accession number $29155 (see entry WTHUB); as a secondary sequence, it should be considered less than fully reliable
                                                                                                                                                                                                                                                                                                 ##molecule_type protein
##residues 105-107,'K',109-111;113-122;260-269;280-283 ##label KIS
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                                                                                                                                                                                                                                                                                                                                                                                                             proteins in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #domain signal sequence #status predicted #label SIGN
#product semenogelin II #status predicted #label MATN
#binding_site carbohydrate (Asn) (covalent) #status
predicted #molecular-weight 65444 #checksum 9704
                                      ##molecule_type protein
##residues 390,'E',392-396,'E',398-400,'EW',403-405,'C',407,'DE'
##label SCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #superfamily semenogelin duplication; glycoprotein; semen; seminal vesicle; tandem
                                                                                                                                                                              Kise, H.; Nishioka, J.; Kawamura, J.; Suzuki, K.
Bur. J. Biochem. (1996) 288:889-96
Characterization of semenogelin II and its molecular
interaction with prostate-specific antigen and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T01344 #type complete
hypothetical protein F6N15.5 - Arabidopsis thaliana
#formal_name Arabidopsis thaliana #common_name mouse-ear
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                                                                                         this report is of a secondary sequence determined
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##cross-references EMBL:AF069299; NID:g3193311; PID:g3193321
                                                                                                                                                                                                                                                                                                                                                                                       Eur. J. Biochem. (1996) 238:48-53
Isolation and characterization of the major gel
human semen, semenogelin I and semenogelin II.
568/62
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##molecule_type DNA
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submitted to the EMBL Data Library, May 1998
The sequence of A. thaliana F6N15.
T01344
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##residues 420-421,'G',423-423 ##label MAL
occurring in human seminal plasma $229156
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Pred. No. 1.66e-01;
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##cross-references GDB:132657; OMIM:182141
Ap_position 20q12-20q13.1
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#map_position IV
#introns 50/2; 342/3; 399/3; 496/2
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#accession S68765
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Best Local Similarity 100.0%;
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Differential expression of isoforms of PSD-95 binding protein (GKAP/SAPAP1) during rat brain development. T00025
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Satch, K.; Yanai, H.; Senda, T.; Kohu, K.; Nakamura, T.;
Okumura, N.; Matsumine, A.; Kobayashi, S.; Toyoshima, K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genes to Cells (1997) 2:415-424
DAP-1, a novel protein that interacts with the guanylate
kinase-like domains of hDLG and PSD-95.
T00013
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PSD-95 binding protein - rat
#formal_name Rattus norvegicus #common_name Norway rat
22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change
22-Jan-1999
                                                                                                                                                                                                                                                                                                                                                          T00013 #type complete
DAP-1 beta protein - human
#formal_name Homo sapiens #common_name man
19-Jan-1999 #sequence_revision 19-Jan-1999 #text_change
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##residues
##reross-references EMBL:AB003594; NID:d1177606; PID:d1025176
SUMMARY #length 692 #molecular-weight 76991 #checksum 9411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##status preliminary
##residues 1-675 ##label SAT ##cross-references BMBL:AB000276; NID:d1173041; PID:d1024134
##cross-references BMBL:AB000276; NID:d1173041; PID:d1024134
!! #elength 675 #molecular-weight 75260 #checksum 1624
#length 509 #molecular-weight 58562 #checksum 4630
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                                                       Score 42; DB 2; Length 509,
Pred. No. 1.20e+00;
1; Mismatches 0; Indels
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DAP-1 alpha protein - human
#formal_name Homo sapiens #common_name man
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                                                             93.3%;
Similarity 85.7%;
6; Conservative
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Query Match 88.9%;
Best Local Similarity 71.4%;
Matches 5; Conservative
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Best Local Similarity 100.0%;
Matches 6; Conservative
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CLASSIFICATION #*
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Bur. J. Biochem. (1995) 233:864-872
Carotene desaturation is linked to a respiratory redox pathway in Narcissus pseudonarcissus chromoplast membranes: involvement of a 23-kba oxygen-evolving-complex-like
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                                                                                                            Satoh, K.; Yanai, H.; Senda, T.; Kohu, K.; Nakamura, T.;
Okumura, N.; Matsumine, A.; Kobayashi, S.; Toyoshima, K.;
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NAD(P)H-quinone oxidoreductase, 23K, precursor - Narcissus
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experimental #label TNP\
#product NAD(P)H-quinone oxidoreductase, 23K #status
experimental #label MAT
                                                                                                                                                             Akiyama, T. Genes to Cells (1997) 2:415-424
DAP-1, a novel protein that interacts with the guanylate kinase-like domains of hDLG and PSD-95.
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ATP-binding protein msmK homolog - Mycoplasma genitalium
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19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change
17-Mar-1999
853532: 863488; 854136
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19-Jan-1999 #sequence_revision 19-Jan-1999 #text_change
                                                                                                                                                                                                                                                                                                    ##status preliminary
##residues 1-977 ##label SAT
##cross-references EMBL:AB000277; NID:d1173042; PID:d1024135
RY #length 977 #molecular-weight 108872 #checksum 4168
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##residues 80-89;93-106;128-148;170-175;247-249 ##label NIW
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2; Mismatches 0
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#accession S63532
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llarity 85.7%;
Conservative
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Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.; Bult, C.J.; Kerlavage, A.R.; Sutton, G.; Kelley, J.M.; Fritchman, J.L.; Weidman, J.F.; Small, K.V.; Sandusky, M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.M.; Tomb, J.F.; Dougherty, B.A.; Bott, K.F.; Hu, P.C.; Lucier, T.S.; Peterson, S.N.; Smith, H.O.; Hutchison III,
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#title The heterogeneity of the polymeric intracellular hemoglobin of Glycera dibranchiata and the cDNA-derived amino acid sequence of one component.
#cross-references WUID:91091412
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#formal_name Glycera dibranchiata #common_name bloodworm
19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change
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                     17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 17-Jul-1998
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#title The minimal gene complement of Mycoplasma genitalium.
#cross-references MUID:96026346
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#length 147 #molecular-weight 16029 #checksum 7221
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#region nucleotide-binding motif A (P-loop)
#length 585 #molecular-weight 66948 #checksum
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Pred. No. 4.25e+00;
2; Mismatches 0; Indels
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#formal_name Mycoplasma genitalium
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##molecule_type mRNA
##residues 1-147 ##label ZAF
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probable Mg2+ transport protein (mgtC) - syphilis spirochete #formal_name Treponema pallidum subsp. pallidum #common_name syphilis spirochete 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change G71281
                                                                                                                                                          Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwinn, M.; Hickey, E.K.; Clayton, R.; Ketchum, K.A.; Sodergren, E.; Hardham, J.M.; McLeod, M.P.; Salzberg, S.; Peterson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDonald, L.; Artiach, P.; Bowman, C.; Cotton, M.D.; Fujii, C.; Garland, S.; Hatch, B.; Horst, K.; Roberts, K.; Watthey, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science (1998) 281:375-388
Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##residues 1-224 ##label COL ##cross-references GB:AEO01249; GB:AEO00520; NID:g3323083; PID:g3323084 ##experimental_source strain Nichols
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The HRASI gene cluster: two upstream regions recognizing the HRASI gene cluster: two third encoding a gene with a leucine
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3; Mismatches 0; Indels
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#accession B44478
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Similarity 85.7%;
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Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                   #Authors Visser, E.S.; McGuire, T.C.; Palmer, G.H.; Davis, W.C.; Shtap, V.; Pipano, E.; Knowles Jr., D.P.
Shtap, V.; Pipano, E.; Knowles Jr., D.P.
#journal Infect. Immun. (1992) 60:5139-5144
#title The Anaplasma marginale msp5 gene encodes a 19-kilodalton protein conserved in all recognized Anaplasma species.
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##molecule_type nucleic acid
##residues 1-210 ##label VIS
##cross-references GB:M93392; GB:S50594; NID:g1209237; PID:g1209238
##note extracted from NCBI backbone (NCBIN:119452, NCBIP:119454)
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#length 585 #molecular-weight 65455 #checksum 7460
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                                                                                           probable membrane protein b1410 - Escherichia coli
#formal_name Escherichia coli
12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change
13-Nov-1998
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#title The complete genome sequence of Escherichia coli K-12.
#cross-references MUID:97426617
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Pred. No. 1.44e+01;
2; Mismatches 1; Indels
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Pred. No. 7.87e+00;
2; Mismatches 0; Indels
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#length 210 #molecular-weight 23132
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J. Blol. Chem. (1994) 269:33079-23086
A cytochrome ba-3 functions as a quinol oxidase in Paracoccus denitrificans. Purification, cloning, and sequence
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                                                                                 "ERENCE A44478
#authors Weitzel, J.N.; Kasperczyk, A.; Mohan, C.; Krontiris, T.G.
#journal Genomics (1992) 14:309-319
#title The HRSI gene cluster: two upstream regions recognizing transcripts and a third encoding a gene with a leucine zipper domain.
#cross-references MUID:93052330
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#formal_name Homo sapiens #common_name man
04-bec-1986 #sequence_revision 03-oct-1995 #text_change
               #formal_name Homo sapiens #common_name man
10_1un-1993 #sequence_revision 18-Nov-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #formal_name Paracoccus denitrificans
28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change
09-Sep-1997
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A43412
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(alternatively spliced type I transcript) - human
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##TOSIGUES
##COSS-references GB:X78196; NID:9461327; PID:9673470
##note it is uncertain whether Met-1 or Met-21 is
initiator; Met-21 seems more likely
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                                                                                                                                                                                                                                                                                                                                                                         Length 373;
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Pred. No. 1.44e+01;
3; Mismatches 0
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ilarity 57.1%;
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Best Local Similarity 57.1%;
Matches 4; Conservative
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#authors Lilja, H.; Abrahamsson, P.A.; Lundwall, A.
#journal J. Biol. Chem. (1989) 254:1980 and Semenogelin, the predominant protein in human semen. Primary structure and identification of closely related proteins in the male accessory sex glands and on the spermatozoa.
#cross-references wilD:89109215
#accession A31489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lilja, H.; Jeppsson, J.O.
FEBS Lett. (1985) 182:181-184
Amino acid sequence of the predominant basic protein in human
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#title Partial amino acid sequence of a human seminal plasma peptide #cross-references MUID:84132557
#accession A91320
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peptide with inhibin-like activity.
#cross-references MUID:84146751
Ulvsback, M.; Lazure, C.; Lilja, H.; Spurr, N.K.; Rao, V.V.; Loffler, C.; Hansmann, I.; Lundwall, A.
J. Biol. Chem. (1992) 267:18080-18084
Gene structure of semenogelin I and II. The predominant proteins in human semen are encoded by two homologous genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #accession A91335
#accession ##molecule_type protein
##molecule_type protein
##residues 108-159 ##label LIZ
##roste this sequence represents a naturally occurring fragment
##note this sequence represents a naturally occurring fragment
from proteolytic cleavage of semenogelin during
liquefaction of semen
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from proteolytic cleavage of semenogelin during
liquefaction of semen
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Manjunath, P.; Schiller, P.W.; Yamashiro, D.; Li, C.H.
Science (1984) 223:1199-1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oţ
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Schneider, K.; Kausler, W.; Tripier, D.; Jouvenal, K.; Spiteller, G.
Biptieller, G.
Biol. Chem. Hoppe-Seyler (1989) 370:353-356
Isolation and structure determination of two peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##molecule_type protein
##residues 316.320, T.', 322-344 ##label SCH
##rote this sequence represents the amino end of a nat
this sequence represents the amino end of a nat
this securing fragment from proteclytic cleavage
semenogelin during liquefaction of semen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1-78,'T',80-422,'K',424-462 ##label LIL
                                                                                                                                                                                                                                                                                                                  ##residues 1-462 ##label ULV
##cross-references GB:M81650; NID:g307416; PID:g487420
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##note Ser-79 was also found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##molecule_type protein
##residues 108-138 ##label RAM
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##residues 108-138 ##label SEI
                                                                                                                                                                              on chromosome 20.
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#accession B43412
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#cross-references MUID:85127550
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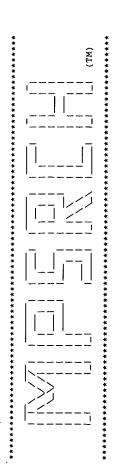
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the amidated tripeptide Glp-Glu-Pro-NH2 (where Glp is pyroglutamic acid) is present in human semen; although the sequence reported here is consistent with an amino-terminally extended form derived from semenogelin, the sequence is followed in semenogelin by Trp, which (unlike Gly) probably cannot become the source of an amide moiety; the authors conclude the peptide must be derived from a closely related protein
                                                                                                                                                                                                    ##molecule_type protein
##molecule_type protein
##residues
##residues
the authors' suggestion that this peptide is amidated is
##note
consistent with radioimmunoassay results but has not
Khan, Z.; Smyth, D.G.
Eur. J. Biochem. (1993) 212:35-40
Isolation and identification of N-terminally extended forms of 5-oxoproly/glutamylprolinamide (Glp-Glu-Pro-NH(2)), a thyrotropin-releasing-hormone(TRH)-like peptide present in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Isolation and characterization of the major gel proteins in
human semen, semenogelin I and semenogelin II.
S68761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #domain signal sequence #status predicted #label SIG\
#product seminal basic protein #status experimental
#label MAT\
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##residues 49-50, @',52-53 ##label MAL
##residues
WT This abundant protein from seminal vesicle secretions maintains
gel-like environment for the sperm cells. At ejaculation,
kallikrein-like enzymes in prostatic secretions cleave this
protein, resulting in liquefaction of the seminal gel and
allowing increased sperm motility.
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#region semenogelin short repeat 2\
#region semenogelin long repeat 1\
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#region semenogelin short repeat 3\
#binding_site carbohydrate (Asn) (covalent) #status
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Pred. No. 1.44e+01;
1; Mismatches 0; Indels
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#cross-references MUID:93185635
#accession $29380
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FEATURE
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Search completed: Thu Oct 28 11:25:08 1999 Job time: 16 secs.

229 EHSSKVQ 235 EHSSKLQ 7

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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Oct 28 11:25:25 1999; MasPar time 2.07 Seconds 95.556 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-081-707-10 (1-7) from US09081707.pep 45 Description: Perfect Score:

1 EHSSKLQ 7 Sequence:

Scoring table:

77977 seqs, 28268293 residues PAM 150 Gap 15 Searched:

Post-processing: Minimum Match 08 Listing first 45 summaries

swiss-prot37 1:swissprot Database:

Mean 19.321; Variance 15.201; scale 1.271 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Pred. No.	3.12e-02	3.12e-02	5.99e-01	1.21e+00	2.43e+00	2.43e+00	2.43e+00	2.43e+00	4.80e+00	4.80e+00	9.35e+00	9.35e+00	9.35e+00	1.79e+01	1.79e+01	1.79e+01	1.79e + 01	1.79e + 01	1.79e + 01	1.79e+01	1.79e+01	1.79e+01	1.79e+01
	Description	SEMENOGELIN II PRECURS		DYSTROPHIN-RELATED PRO	HYPOTHETICAL ABC TRANS	KRUEPPEL HOMOLOGOUS PR	GLOBIN, MAJOR POLYMERI	PEROXISOME ASSEMBLY PR	MYOSIN IJ HEAVY CHAIN.	SEMENOGELIN I PROTEIN	HYPOTHETICAL 88.2 KD P	HYPOTHETICAL 10.2 KD L	PEPTIDE CHAIN RELEASE	NONSTRUCTURAL POLYPROT	GLOBIN, POLYMERIC COMP	40S RIBOSOMAL PROTEIN	REGULATORY PROTEIN OCC	ATP SYNTHASE GAMMA CHA	HYPOTHETICAL 37.3 KD P	DIMETHYLANILINE MONOOX	PROBABLE DNA PACKAGING	SYNAPTONEMAL COMPLEX P	HYPOTHETICAL 150.8 KD	DYNEIN BETA CHAIN, CIL
SUMMARIES	Ω	SEM2_HUMAN	SEM2_MACMU	DRP2_HUMAN	Y187_MYCGE	KRUH_DROME	GLP1_GLYDI	PEX2_YARLI	MYSJ_DICDI	SEM1_HUMAN	YA2I_SCHPO	YPDI_ECOLI	RF1_BACSU	POLN_RRVN	GLP3_GLYDI	RS2_DICDI	OCCR_AGRI6	ATPG_HELPY	Y070_MYCTU	FMO3_RABIT	VTER_HSV11	ZIP1_YEAST	YBE7_YEAST	DYHC_ANTCR
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dР	Query Match	100.0	100.0	91.1	88.9	86.7	86.7	86.7	86.7	84.4	84.4	82.2	82.2	82.2	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0
	Score	45	45	41	40	39	39	39	39	38	38	37	37	37	36	36	36	36	36	36	36	36	36	36
	Result No.	-	8	М	4	2	9	7	ထ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

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BROLACHT I PRECITESOR		BETA-1,4 N-ACETYLGALAC	HPR1 PROTEIN.	WIDE HOST RANGE VIRA P	EUKARYOTIC INITIATION	P53-BINDING PROTEIN 53	KINESIN-LIKE PROTEIN K	HYPOTHETICAL 128.6 KD	CITRON PROTEIN.	DNA-DIRECTED RNA POLYM	DNA-DIRECTED RNA POLYM	MONOCYTIC LEUKEMIA ZIN	CELL DIVISION-ASSOCIAT	NONSTRUCTURAL POLYPROT	NONSTRUCTURAL POLYPROT	LAMININ ALPHA-1 CHAIN	HYPOTHETICAL 7.7 KD PR	HYPOTHETICAL 51.1 KD P	VACUOLAR ASSEMBLY PROT	HYPOTHETICAL PROTEIN K	HYPOTHETICAL 229.9 KD
PRI.1 OREMO	IPPI_SCHPO	CAG2_HUMAN	HPR1_YEAST	VIRA_AGRT5	IF41_YEAST	P532_HUMAN	KIP1_YEAST	YO60_CAEEL	CTRO_MOUSE	RPA1_RAT	RPA1_MOUSE	MO2_HUMAN	BIMB_EMENI	POLN_SFV	POLN_ONNVG	LMA1_MOUSE	Y7K7_BPP22	YAJB_SCHPO	VP39_YEAST	Y133_HUMAN	YJU7_YEAST
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212	227	533	752	833	952	1005	1111	1139	1597	1716	1717	2004	2067	2431	2514	3084	69	442	1049	1524	2014
77.8	77.8	77.8	77.8		77.8	77.8	77.8	77.8	77.8	77.8	77.8	77.8	77.8	77.8	77.8	77.8	75.6	75.6	75.6	75.6	75.6
35	35	35	32	32	35	32	35	32	32	35	32	35	32	35	35	35	34	34	34	34	34
24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

?			(3)	•		MAMMALIA; EUTHERIA;						of epididymal and seminal vesicular transcripts		1992).				N.K., KAO V.V., LOEFFLER C.,	100000000000000000000000000000000000000	predominant procesus	( 100 our our our or	FUNCTION: THREE SEMENOGELIN PROTEINS ARE FOUND IN HUMAN SEMEN.	OF WHICH THE 52 KD SEMENOGELIN I IS THE MOST ABUNDANT. THEY	PARTICIPATE IN THE FORMATION OF A GEL MATRIX ENTRAPPING THE	ACCESSORY GLAND SECRETIONS AND EJACULATED SPERMATOZOA. FRAGMENTS	OF THE RELATED PROTEINS MAY	CONTRIBUTE TO THE ACTIVATION OF PROGRESSIVE SPERM MOVEMENTS AS	GEL-FORMING PROTEINS ARE FRAGMENTED BY THE KALLIKREIN-LIKE	FROLIDADE. SIDILINIE DIEMIDINE INVED COMDIEVES OF SEMENOCEINS IN MUS OMUSE	SEMENOGELIN I AND THE CIRER	OLITION THE SPECIFIC THY SEMINAL VESTICES. AND TO A MICH TESSER		SEMENOGELIN II IS THOUGHT TO FORM BOTH THE 71-KD POLYPEPTIDE	AND, IN ITS GLYCOSYLATED FORM, THE 76-KD POLYPEPTIDE.		This SWISS-PROT entry is copyright. It is produced through a collaborati	ics and the EMBL outstation	are no restrictions	as its content is in no w	Usage by and tor commerci
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	PRT;	CREATED) .	35, LAST ANNOTATION UPDATE)	SGII).		TA; VERTEBR	VIDAE; HOMO					idymal and	semenogelin-related protein.	.A. 89:4559			:	LLJA H., SP	And I and	tio bomolo	3084 (1992)	SELIN PROTE	SNOGELIN I	MATION OF A	CONS AND EJ	SEMENOGELIN AND/OR FRAGMENTS OF	ATION OF P.	S ARE FRAG	אים זמאורים, רופי	NED COMPLEX	TINAL VESTO		THOUGHT TO	ED FORM, TH.		opyright. I	e of Bioin	Institute	utions as	and this statement is not removed.
	STANDARD;	, CREATED)	, LAST	II PRECURSOR (SGII).		CHORDA	; HOMI		į	, 21		f epid	in-rel	I. U.S.			,	ة : :	L A.;	מוניונים לייני	8080-15	SEMENOC	KD SEME	HE FORM	SECRETI	ND/OR I	E ACTIV	PROTEIN	INT I TO	TING THE	TV SER	IS.	II IS	OSYLATE		y is co	nstitut	rmatics	instit	atemenı
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LT 1	SEM2_HUMAN	01-JUL-1993	01-NOV-1997	SEMENOGELIN	SEMGZ: HOMO SAPIENS (HUMAN)	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;	PRIMATES; CATARRHINI; HOMINIDAE; HOMO.	[1]	SEQUENCE FROM N.A.	MEDITAR: 922		"Molecular cloning	encoding a s	PROC. NATL. ACAD. SCI. U.S.A. 89:4559-4563(1992).	[2]		MEDLINE; 923	ULVSBAECK M., LAZUKE C., LILUA H., SPUKK	HANSMANN I., EUNDWALL A.; "Cope structure of comescents I and II mho	biman comen are	J. BIOL. CHEM. 267:18080-18084/1992)	- ! - FUNCTION	OF WHICH	PARTICIP	ACCESSOR	OF SEMEN	CONTRIBU	THE GEL-F	- CTIBITATE		-i- TISSUE S		-! - PTM: SEM	AND, IN		This SWISS-P	between the	the European	use by non-profit institutions as long as	modified and
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- FUNCTION: PARTICIPATE IN THE FORMATION OF A GEL MATRIX ENTRAPPING
THE ACCESSORY GLAND SECRETIONS AND EJACULATED SPERMATOZOA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ULYSBACK M., LUNDWALL A.; "Cloning of the rhesus monkey. "Cloning of the semenogelin II gene of the region in man, rhesus monkey Duplications of 360 bp extend the coding region in man, rhesus monkey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; CERCOPITHECIDAE; CERCOPITHECINAE; MACACA.
                                                                                                                                                                                                                                                   2-1.
2-2.
4 x 60 AA TANDEM REPEATS, TYPE I.
3-2.
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                                                                                                                                                                                                                                                                                                                                                                                   Score 45; DB 1; Length 582;
Pred. No. 3.12e-02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                      EMBL; M81652; G338239; -.
EMBL; Z47556; E82662; -.
PIR; A43412.
MIM; 182141; -.
SEMEN; SEMINAL VESICLE; REPEAT; SIGNAL; GLYCOPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEMEN, SEMINAL VESICLE, REPEAT, SIGNAL, GLYCOPROTEIN SIGNAL
                                                                                                                                                                                          SEMENOGELIN II.
REPEAT-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEMENOGELIN II. 9D5897A8 CRC32;
                                                                                                                                                                                                                                                                                                                                                 65445 MW; DD20304E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-UD-1998 (REL. 36, LAST ANNOTATION UPDATE)
SEMENOGELIN II PRECURSOR (SGII).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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79875 MW;
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                      EMBL; M81651; G307418; -.
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582 AA;
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EHSSKLQ 7
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REPEAT
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                                                                                                                                                                                                                                                                                                      MEDLINE; 96225452.

ROBERTS R.G., FREEMAN T.C., KENDALL E., VETRIE D.L.P., DIXON A.K., SHAW-SMITH C., BONE Q., BOBROW M.;

"Characterization of DRP2, a novel human dystrophin homologue.";

NAT. GENET. 13:223-226(1996).

-!- FUNCTION: POSSIBLY INVOLVED IN MEMBRANE-CYTOSKELETON INTERACTIONS OF THE CENTRAL NERVOUS SYSTEM.

-!- TISSUE SPECIFICITY: BRAIN AND SPINAL CORD: VERY LOW LEVELS IN EYE, OVARY, EPIDLIDYMIS AND TESTIS: NOT IN CARRIAGE AND SKELETAL MUSCLE.

-!- SIMILARITY: IN OVERALL STRUCTURE TO DP116 DYSTROPHIN ISOFORM.
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0
                                                                                                                                           HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; MOLLICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41; DB 1; Length 954; Pred. No. 5.99e-01;
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01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST SANGTATION UPDATE)
HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MG187.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0197AA02 CRC32;
01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANOTATION UPDATE)
DYSTROPHIN-RELATED PROTEIN 2.
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EF-HAND.
EF-HAND.
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2.
WW DOMAIN.
ZZ DOMAIN.
TO EF-HAND.
TO EF-HAND.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM; 300052; -.
PROSITE; PS01159; WW_DOMAIN_1; 1.
PROSITE; PS50020; WW_DOMAIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOSKELETON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107673 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM: PF00397; WW_rsp5_WWP; 1.
PFAM: PF00435; spectrin; 2.
PFAM: PF00569; ZZ; 1.
STRUCTURAL PROTEIN: CTTOSKELET
CA BIND 20 31
REPEAT 98 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MYCOPLASMATACEAE; MYCOPLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91.1%;
Similarity 71.4%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U43519; G1353782; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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380
648
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500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       954 AA;
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99 DHSGKLQ 105
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Gaps

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0; Indels

Length 79;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBUNIT: POLYMER.
-!- THIS PROTEIN IS ONE OF AT LEAST SIX COMPONENTS IN THE POLYMERIC
FRACTION OF GLYCERA HEMOGLOBIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUKARYOTA; METAZOA; ANNELIDA; POLYCHAETA; PHYLLODOCIDA; GLYCERIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 91091412. STERN M.S., VINOGRADOV S.N., WALZ D.A.; ASPAR R.S., CHOW L.H., STERN M.S., VINOGRADOV S.N., WALZ D.A.; "The heterogeneity of the polymeric intracellular hemoglobin of Glycera dibranchiata and the cDNA-derived amino acid sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND SEQUENCE OF 1-27; 98-102 AND 119-145.
MEDLINE; 91091412.
                                                 DNA-BINDING; REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 39; DB 1; Le
Pred. No. 2.43e+00;
0; Mismatches 0
                                                                                                                                                                                                                                                              Score 39; DB 1; L
Pred. No. 2.43e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OXYGEN TRANSPORT; RESPIRATORY PROTEIN.
NCE 147 AA; 16019 MW; 61C9888B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1991 (REL. 20, CREATED)
01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                     3B8448AF CRC32;
                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     380 AA
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01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
                                                                                       ZINC-FINGERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BIOCHIM. BIOPHYS. ACTA 1041:117-122(1990)
                                                                                                                                                      C2H2-TYPE.
C2H2-TYPE.
                                                                                                              C2H2-TYPE.
C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLOBIN, MAJOR POLYMERIC COMPONENT PI.
GLYCERA DIBRANCHIATA (BLOODWORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS01033; GLOBIN; 1.
                                               ZINC-FINGER; METAL-BINDING;
                                                                                                                                                                                                                     9544 MW;
                                                                                                                                                                                                                                                              86.7%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity 100.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86.78;
    PFAM; PF00096; zf-C2H2; 2.
HSSP; P08047; 1SP2.
                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM; PF00042; globin; 1. HSSP; P02216; 1HBG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; S13157; S13157
                                                                                                                                                                                                                                                                                                                                                     49 EHSGKLH 55
                                                                                                                                                                                                                                                                                                                                                                              |||:||:
| EHSSKLQ 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62
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2 HSSKLQ 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             LT 6
GLP1_GLYDI
P23216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEX2_YARLI
Q99155;
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NON_TER
SEQUENCE
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ZN_FING
ZN_FING
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                                                                       NON_TER
                                                                                         DOMAIN
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               MEDLINE; 96026346.
FRASER C.M., GOCAYNE J.D., WHITE O., ADAMS M.D., CLAYTON R.A.,
FLEISCHMANN R.D., BULT C.J., KERLAYAGE A.R., SUTTON G., KELLEY J.M.,
FRITCHMANN J.L., WEIDMAN J.F., SMALL K.V., SANDUSKY M., FUHRANNN J.L.,
NGUYEN D.T., UTTERBACK T.R., SAUDEK D.M., PHILLIPS C.A., MERRICK J.M.
TOMB J.-F., DOUGHERTY B.A., BOTT K.F., HU P.-C., LUCIER T.S.,
PETERSON S.N., SMITH H.O., HUTCHISON C.A. III, VENTER J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              segmentation gene.";
CELL 47:1025-1032(1986).
-!- SIMILARITY: BELONGS TO THE KRUEPPEL SUBFAMILY OF C2H2-TYPE ZINC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                 "The minimal gene complement of Mycoplasma genitalium.";
SCIENCE 270:397-403(1995).
-!- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE: 87051757.
SCHUH R., AICHER W., GAUL U., COTE S., PREISS A., MAIER D.,
SEHERT E., NAUBER U., SCHRODER C., KEMLER R., JACKLE H.;
"A conserved family of nuclear proteins containing structural
elements of the finger protein encoded by Kruppel, a Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DROSOPHILA MELANOGASTER (FRUIT FLY).
EUKARYOTA: METAZOA; ARTHROPODA: TRACHEATA; HEXAPODA; INSECTA;
PTERYGOTA: DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40; DB 1; L
Pred. No. 1.21e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FC78C4B8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00211; ABC_TRANSPORTER; 1.
PFAM; PF00005; ABC_tran; 1.
HYPOTHETICAL PROTEIN; ATP-BINDING; TRANSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1988 (REL. 08, CREATED)
01-AUG-1988 (REL. 08, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FLYBASE; FBGN0001326; Kr-h.
PROSITE; PS00028; ZINC_FINGER_C2H2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KRUEPPEL HOMOLOGOUS PROTEIN (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      585 AA; 66949 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 71.4%;
5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DROSOPHILIDAE; DROSOPHILA
STRAIN=ATCC 33530 / G-37;
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                                                                                                                                                                                                                                       (ABC TRANSPORTERS).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
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KRUH_DROME
P08155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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Length 147;

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STANDARD;
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866
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284
291
347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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865
2245
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191
284
291
332
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1 EHSSKLQ 7
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  S THE FETTE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                         MEDLINE; 9635553.
ETZEN G.A., TITOENKO V.I., SMITH J.J., VEENHUIS M.,
SZILARD R.K., RACHUBINSKI R.A.;
"The Yarrowia lipolytica gene PAY5 encodes a peroxisomal integral
                                                                        YARROWIA LIPOLYTICA (CANDIDA LIPOLYTICA).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
                                                                                                                                                                                                                                                                                                          membrane protein homologous to the mammalian peroxisome assembly factor PAF-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                PEROXISOMES (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. PEROXISOMAL
                                                                                                                                                                                                                                                                                                                                                                BIOL. CHEM. 271:20300-20306(1996).
FUNCTION: REQUIRED FOR THE IMPORT OF SEVERAL PROTEINS INTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C3HC4-TYPE.
POLY-GLY.
ASP/GLU-RICH (HIGHLY ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 39; DB 1; Length 380;
Pred. No. 2.43e+00;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [2]
SEQUENCE OF 1-1021 FROM N.A.
PETERSON M.D., TITUS M.A.,
SUBMITTED (JAN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAMMER J.A. III, JUNG G.;
SUBMITTED (JAN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        489F7120 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-00T-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
LAST ANNOTATION UPDATE)
                     PEROXISOME ASSEMBLY PROTEIN PAYS (PEROXIN-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 2245 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
EUKARYOTA; DICTYOSTELIIDA; DICTYOSTELIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U43081; G1209744; -.
PROSTIE; PS00518; ZINC_FINGER_C3HC4; 1.
PFAM; PFO0097; Zf-C3HC4; 1.
TRANGMEMBRANE; PEROXISOME; ZINC-FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-GLU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42727 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 182-298 FROM N.A. MEDLINE; 9,5023928.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                              DIPODASCACEAE; YARROWIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MYOSIN IJ HEAVY CHAIN.
  01-NOV-1997 (REL. 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153
208
265
277
354
360
367
380 AA;
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                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111111
2 HSSKLQ 7
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TRANSMEM
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DOMAIN
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ULVSBAECK M., LAZURE C., LILJA H., SPURR N.K., RAO V.V., LOEFFLER C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LILLA H., ABRAHAMSON P.-A., LUNDWALL A.;
"Semenogelin, the predominant protein in human semen. Primary
structure and identification of closely related proteins in the male
accessory sex glands and on the spermatozoa.";
J. BIOL. CHEM. 264:1894-1900(1989).
TITUS M.A., KUSPA A., LOOMIS W.F.;
"Discovery Of myosin genes by physical mapping in Dictyostelium.";
"Discovery Of myosin genes by physical mapping in Dictyostelium.";
PROC. NATL. ACAD. SCI. U.S.A. 91:9446-9450(1994).
-!- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO ACTIN AND HAS ATPASE
-ACTIVITY THAT IS ACTIVATED BY ACTIN.
-!- SUBJUNIT: HOMODIMER (POTEWITH).
-!- SIMILARITY: BELONGS TO CLASS-5 MYOSINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L -> F (IN REF. 2).
A -> T (IN REF. 2).
G -> R (IN REF. 2).
NKSGCPEIEGVSDEEH -> IEWMFELKVYRMKS (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MYOSIN; REPEAT; ATP-BINDING; CALMODULIN-BINDING; ACTIN-BINDING; HEPTAD REPEAT PATTERN; COILED COIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANDUDATION UPDATE)
SEMENGELIN I PROTEIN PRECURSOR (SGI) [CONTAINS: SEMINAL BASIC PROTEIN, ALPHA-INHIBIN-92; ALPHA-INHIBIN-31].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2245;
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COILED COIL (POTENTIAL).
TAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ).
((IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HH -> QQ (IN REF. 2
MW; 48F462D8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 39; DB 1; Lo Pred. No. 2.43e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP (POTENTIAL). ACTIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               462 AA.
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N -> K (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFAM; PF00063; myosin_head; 2.
PFAM; PF00612; IQ; 3.
HSSP; P08799; 1MND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86.7%;
llarity 71.4%;
Conservative
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EMBL; L35322; G1039361; -.
DICTYDB; DD01095; MYOJ.
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Gaps

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Indels

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Mismatches

Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                        PROC. NATL. ACAD. SCI. U.S.A. 82:4041-4044(1985).

-1- FUNCTION: SEMENOGELIN I IS THE PREDOMINANT PROTEIN IN HUMAN SEMEN.

IT PARTICIPATES IN THE FORMATION OF A GEL MATRIX ENTRAPPING THE
ACCESSORY GLAND SECRETIONS AND EJACULATED SPERMATOZOA. FRAGMENTS
OF SEMENOGELIN AND/ON FRAGMENTS OF THE RELATED PROTEINS MAY
CONTRIBUTE TO THE ACTIVATION OF PROGRESSIVE SPERM MOVEMENTS AS
THE GEL-FORMING PROTEINS ARE FRAGMENTED BY THE KALLIRREIN-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: ALPHA-INHIBIN-92 AND ALPHA-INHIBIN-31, DERIVED FROM THE PROTECLYTIC DEGRADATION OF SEMENOGELIN, INHIBIT THE SECRETION OF PITUITARY FOLLICLE-STIMULATING HORMONIT.
SUBUNIT: OCCURS IN DISCLEDE-LINKED COMPLEXES WHICH MAY ALSO CONTAIN TWO LESS ABUNDANT 71- AND 76-KD SEMENOGELIN-RELATED
         "Gene structure of semenogelin I and II. The predominant proteins in human semen are encoded by two homologous genes on chromosome 20."; J. BIOL. CHEM. 267:18080-18084(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 AA REPEAT 1.

42 AA REPEAT 2.

58 AA REPEAT 1.

58 AA REPEAT 2.

42 AA REPEAT 3.

5 -> T (LESS COMMON GENETIC VARIANT).

K -> N (IN REF. 2).

W; C87515C7 CRC32;
                                                                                                                                                                             SEIDAH N.G., RAWASHARWA K., SAIRAM M.R., CHRETIEN M.; "Partial amino acid sequence of a human seminal plasma peptide with inhibin-like activity."; inhibin-like activity."; FEBS LETT. 167:98-102(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEMENOGELIN I.
PYRROLIDONE CARBOXYLIC ACID (PROBABLE).
ALPHA-INHIBIN-92.
                                                                                                                                                                                                                                                                     LI C.H., HAMMONDS R.G., RAMASHARMA K., CHUNG D.;
"Human seminal alpha inhibins: isolation, characterization, and
                                                                                                "Amino acid sequence of the predominant basic protein in human seminal plasma.";
FEBS LETT. 182:181-184(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEMEN; SEMINAL VESICLE; REPEAT; SIGNAL; POLYMORPHISM SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALPHA-INHIBIN-31.
SEMINAL BASIC PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 38; DB 1; I
Pred. No. 4.80e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- TISSUE SPECIFICITY: SEMINAL VESICLE.
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85.78;
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52131
                                                           SEQUENCE OF 108-159.
MEDLINE; 85127550.
LILJA H., JEPPSSON J.-O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; J04440; G338019; -. EMBL; Z47556; E133812; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M81650; G487420; -. PIR; A03254; WTHUB. PIR; A31489; A31489.
HANSMANN I., LUNDWALL A.;
                                                                                                                                                      OF 108-138.
84132557.
                                                                                                                                                                                                                                            SEQUENCE OF 68-159.
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79
423
462 AA;
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                                                                                                                                                                                                                                                                                                   structure.";
                                                                                                                                                      OF.
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PEPTIDE
PEPTIDE
PEPTIDE
DISULFID
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REPEAT
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VARIANT
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
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Length 462;

Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENTLES S., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.; SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-MLZ / MG1655;
MEDIINE: 974261615
BLAITNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,
                                                                                                                                                                                                                                                                                                                                                                                                     HUNT S., DEVLIN K., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37, CREATED)
37, LAST SEQUENCE UPDATE)
37, LAST ANNOTATION UPDATE)
KD LIPOPROTEIN IN EVGS-DDG REGION PRECURSOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 38; DB 1; Length 777; Pred. No. 4.80e+00; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBMITTED (SEP-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
U-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
HYPOTHETICAL 88.2 KD PROTEIN C2F7.18C IN CHROMOSOME
SPACZF7.18C OR SPACI3A11.01C.
                                                                                                                                                                                                                                                                                 EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES; SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE; SCHIZOSACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88207 MW; BDBCAFB7 CRC32;
                                                                                                                        777 AA
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                                                                                                                                                                                                                                                                    SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)
                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 114-777 FROM N.A.
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71.4%;
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-147 FROM N.A.
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                                                                                                                        STANDARD;
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PFAM; PF00611; FCH; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     777 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P01888; 1BMG
                                                                                                                                                             (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL 10.2
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229 EHSSKVQ 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ESCHERICHIA COLI
                         FHSSKLO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL
SEQUENCE 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EHSSKLO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESCHERICHIA.
                                                                                                                                                               01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=972;
                                                                                                                      YA21_SCHPO
Q09697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YPDI_ECOLI
032528;
                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=972
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Gaps

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Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDILINE; 88179556.
FARAGHER S.G., MEEK A.D.J., RICE C.M., DALGARNO L.;
"Genome sequences of a mouse-avirulent and a mouse-virulent strain of Ross River virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The cDNA sequences encoding two components of the polymeric fraction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VIROLOGY 163:509-526(1988).

-I- FUNCTION: NSP2 MAY BE INVOLVED IN RNA BINDING DURING REPLICATION.

-I- PIM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.

-I- READTHROUGH OF THE TERMINATOR CODON UGA OCCURS BETWEEN THE CODONS FOR 1862-PHE AND 1863-LEU.
                                                                                                                                                                                                                                                                                                                                                                                                                                          NONSTRUCTURAL POLYPROTEIN [CONTAINS: NONSTRUCTURAL PROTEINS NSP1 TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUKARYOTA; METAZOA; ANNELIDA; PÓLYCHAETA; PHYLLODOCIDA; GLYCERIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ROSS RIVER VIRUS (STRAIN NB5092) (RRV).
VIRUSES: SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; TOGAVIRIDAE;
ALPHAVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 91072390.
ZAFAR R.S., CHOW L.H., STERN M.S., SCULLY J.S., SHARMA P.R.,
VINOGRADOV S.N., WALZ D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M20162; G1256538; ALT_FRAME.
PIR; A28605; MNWVRA.
POLYPROTEIN; NONSTRÜCTÜRAL PROTEIN; RNA-BINDING; HELICASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 37; DB 1; Length 2479 Pred. No. 9.35e+00; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NONSTRUCTURAL PROTEIN NSP1.
NONSTRUCTURAL PROTEIN NSP3.
NONSTRUCTURAL PROTEIN NSP3.
   red. No. 9.35e+00;
3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CF5E6779 CRC32;
                                                                                                                                                                                                                                                                                                                                      01-JAN-1990 (REL. 13, CREATED)
01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1991 (REL. 18, CREATED)
01-MAY-1991 (REL. 18, LAST SEQUENCE UPDATE)
01-NOV-1991 (REL. 20, LAST ANOTATION UPDATE)
GLOSIN, POLYMERIC COMPONENT P3.
GLYCERA DIBRANCHIATA (BLOODWORM).
                                                                                                                                                                                                                                                                                   2479 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147 AA
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      Pred.
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Best Local Similarity 71.4%;
Matches 5; Conservative
   Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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1332 186
1869 247
2479 AA;
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                                                                                            346 DQASKLQ 352
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1 EHSSKLQ 7
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1 EHSSKLQ 7
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POLN_RRVN
P13887:
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P21660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
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                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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GLASER P., DE LA FUENTE V., DANCHIN A.;
SUBMITTED (MAY-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: PEPTIDE CHAIN RELEASE FACTOR 1 DIRECTS THE TERMINATION OF TRANSLATION IN RESPONSE TO THE PEPTIDE CHAIN TERMINATION CODONS UAG AND UAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE PROKARYOTIC AND MITOCHONDRIAL RELEASE FACTORS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F., GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BACILLUS SUBTILIS.
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
BACILLUS.
                                                                                         "The complete genome sequence of Escherichia coli K-12.";
SCIENCE 277:1453-1474(1997).
-!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
0
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N-ACYL DIGLYCERIDE (POTENTIAL).
294E168F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.2%; Score 37; DB 1; Length 356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 37; DB 1; Length 91;
Pred. No. 9.35e+00;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; ABLOUGE, CT. PROJ. ECOGENE; EG14376; YPDI. ECOGENE; EG14376; YPDI. PROSITE; PSCO0013; PROKAR_LIPOPROTEIN; I. HYPOTHETICAL PROTEIN; MEMBRANE; LIPOPROTEIN; SIGNAL. 18 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40233 MW; 7BFE8DDD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
PEPTIDE CHAIN RELEASE FACTOR 1 (RF-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              356 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00745; RF_PROK_I; 1. PFAM; PF00472; RF-1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995 (REL. 32, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91 AA; 10162 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE000326; G2367134; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.2%;
ilarity 83.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Z49782; G853776; -. EMBL; Z99122; E1184607; - SUBTILIST; BG11244; PRFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18
19
19
                                                                                                                                                                                         ANCHOR (PROBABLE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               356 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                            MAU B., SHAO Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48 HSTKLQ 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1|:|||
2 HSSKLQ 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RF1_BACSU P45872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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CHAIN

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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE: 91319544.

PROFFITT J.A., JAGGER P.S., WILSON G.A., DONOVAN J.T.J.,
WIDDOWSON D. C.C., HAMES B.D.;
Advelopmentally regulated gene encodes the dictyostelium homolog
of yeast ribosomal protein 54 and mammalian LLRep3 proteins.";
NUCLEIC ACIDS RES. 19:3867-3873(1991).

SIMILARITY: BELONGS TO THE S5P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
of the intracellular hemoglobin of Glycera dibranchiata.";
J. BIOL. CHEM. 265:11843-21851(1990).
-!- SUBUNIT: POLYMER.
-!- THIS PROTEIN IS ONE OF AT LEAST SIX COMPONENTS IN THE POLMERIC
FRACTION OF GLYCERA HEMOGLOBIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                       Score 36; DB 1; Length 147; Pred. No. 1.79e+01; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36; DB 1; Length 265;
Pred. No. 1.79e+01;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                    EMBL; M55444; G159147; -.
PIR; B36529; B36529.
PROSITE: PS01033; GLOBIN; 1.
PFAM; PF00042; globin; 1.
HSSP; P02216; 1HBG.
HEME; OXYGEN TRANSPORT; RESPIRATORY PROTEIN.
SEQUENCE 147 AA; 15977 MW; 747D26B7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1992 (REL. 23, CREATED)
01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
40S RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28717 MW; 7A26BB45 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         265 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
EUKARYOTA; DICTYOSTELIIDA; DICTYOSTELIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE: PS00585; RIBOSOMAL_S5; 1. PFAM; PF00333; S5; 1. HSSP; P02357; 1PKP.
                                                                                                                                                                                                                                                                                                                                                                                                       80.0%;
imilarity 83.3%;
5; Conservative
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Best Local Similarity 83.3%;
Matches 5; Conservative
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Matches 5; Conserv
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PROSITE; PS00585;
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2 HSSKLQ 7
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Db 255 EHSAKL 260
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Oct 28 11:25:51 1999; MasPar time 4.17 Seconds 91.547 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-081-707-10 (1-7) from US09081707 pep 45 Title: Description: Perfect Score: Sequence:

1 EHSSKLQ 7

179066 segs, 54579741 residues Searched:

PAM 150 Gap 15

Scoring table:

Post-processing: Minimum Match 08 Listing first 45 summaries

sptremb19 Database:

1:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human 5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle 9:sp\_phage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified 13:sp\_vertebrate 14:sp\_virus

Mean 18.462; Variance 16.244; scale 1.136

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Query Match Length DB	DB	ΙD	Description	Pred. No.
Н	42	93.3	509	10	.081317	F6N15.5 PROTEIN.	8.55e-01
7	42	93.3	627	4	P78335	GUANYLATE KINASE ASSOC	8.55e-01
m	42	93.3	999	H	P97841	GUANYLATE KINASE ASSOC	8.55e-01
4	42	93.3	675	4	014489	DAP-1 BETA.	8.55e-01
ഗ	42	93.3	692	디	054773	PSD-95 BINDING PROTEIN	8.55e-01
9	42	93.3	977	4	014490	DAP-1 ALPHA.	8.55e-01
7	42	93.3	992	11	P97836	PSD-95/SAP90-ASSOCIATE	8.55e-01
ω	42	. 93.3	1548	S	P91339	SIMILARITY TO HUMAN PR	8.55e-01
σ	42	93.3	1638	Ŋ	061529	GUANINE NUCLEOTIDE EXC	8.55e-01
10	42	93.3	2488	Ŋ	061528	GUANINE NUCLEOTIDE EXC	8.55e-01
11	40	88.9		10	040407		3.23e+00
12	40	88.9		~	085281	85KDA STRAIN-SPECIFIC	3.23e+00
13	40	88.9	1	7	066101	AVIRULENCE PROTEIN.	3.23e+00
14	39	86.7	585	~	P76092	FROM BASES 1472112 TO	6.19e+00
15	38	84.4	186	7	075935	DYNACTIN SUBUNIT.	1.17e+01
16	38	84.4	210	~	P70747	MAJOR SURFACE PROTEIN	1.17e+01
17	38	84.4	224	~	083753	MG2+ TRANSPORT PROTEIN	1.17e+01
18	38	84.4	273	14	084175	EARLY-EXPRESSED PROTEI	1.17e+01
19	38	84.4	373	7	002833	PUTATIVE TRANSCRIPTION	1.17e+01
20	38	84.4	402	Ŋ	045858	T27E7.3 PROTEIN.	1.17e+01

1.7 e+01 1.7 e+01 1.7 e+01 1.7 e+01 1.7 e+01 1.7 e+01 1.7 e+01 1.7 e+01 1.8	SIDAE;	. O sd
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CYTOCHROME BA(3) PRECU TEGUNENT PROTEIN. T3K9.25 PROTEIN. TULIP 1. TULIP 1. TULIP 2. TRIP230. TRIP30. TRIP	ALIGNMENTS  IMINARY; PRT; 509 AA.  MBLREL. 08, CREATED)  MBLREL. 08, LAST SEQUENCE UPDATE)  MBLREL. 08, LAST ANNOTATION UPDATE)  JANA (MOUSE-EAR CRESS).  SPERMATOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA; SPERMATOPHYTA; EMBRYOPHYTA; EUDICOTYLEDONS; ROSIDAE SICACEAE; ARABIDOPSIS.  A.  A.  Genome Sequencing Project.";  1 Genome Sequencing Project.";  998) TO EMBL/GENBANK/DDBJ DATA BANKS.  A.  A.  A.  A.  A.  A.  A.  A.  A.	DATA BANKS. RC32; 10; Length 509; 5e-01; es 0; Indels 0
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
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SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
                                                                                                     HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
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J. CELL BIOL. 136:669-678(1997).
ENBL: U67987; G1857139; -.
SEQUENCE 666 AA; 74233 MW; B3E3BB93 CRC32;
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MEDLINE; 97177144.
KIM E., NAISBITT S., HSUEH Y.P., RAO A., ROTHSCHILD A., CRAIG A.M.,
SHENG M.;
                                                                                                                                                                                                                                                        "GKAP, a novel synaptic protein that interacts with the guanylate kinase-like domain of the PSD-95/SAP90 family of channel clustering
                                                                                                                                                                                  MEDLINE; 97177144.
KIM E., NAISBITT S., HSUEH Y.P., RAO A., ROTHSCHILD A., CRAIG A.M.,
SHENG M.;
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Pred. No. 8.55e-01;
1; Mismatches 0; Indels
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Pred. No. 8.55e-01;
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LAST ANNOTATION UPDATE)
  01-MAY-1997 (TREMBLREL. 03, CREATED)
01-MAY-1997 (TREMBLEEL. 03, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
GUANVILLE KINASE ASSOCIATED PROTEIN.
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J. CELL BIOL. 136:669-678(1997).
EMBL: U67988; G1857137, -...
EMBL: T7 AA: 70051 MW; C40A3CBB CRC32;
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01-MAY-1997 (TREMBLREL. 03, LAST SEQ
01-NAY-1998 (TREMBLREL. 08, LAST ANN
GUANYLATE KINASE ASSOCIATED PROTEIN.
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Best Local Similarity 85.7%;
Matches 6; Conservative
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Similarity 85.7%;
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Best Local Similarity
Matches 6; Conser
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SEQUENCE FROM N.A.
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P97841;
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EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
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01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
PSD-95 BINDING PROTEIN.
RATUGS NOWVEGICUS (RAD)
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCIUROGNATHI; MURIDAE; MURINAE; RATUS.
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MEDLINE; 97431353.
MEDLINE; 97431353.
SATOH K., YANAI H., SENDA T., KOHU K., NAKAMURA T., OKUMURA N.,
MATSUMINE A., KOBAYASHI S., TOYOSHIMA K., AKIYAMA T.;
"DAP-1, a novel protein that interacts with the guanylate kinase-like domains of hDLG and PSD-95.";
GENES TO CELLS 2:415-424 (1997).
EMBL; ABO00277; D1024135; -.
SEQUENCE 977 AA; 108872 MW; FFFOAOAO CRC32;
MEDLINE; 97431353.
SATOH K., YANDA T., SENDA T., KOHU K., NAKAMURA T., OKUMURA N.,
MATSUMINE A., KOBAYASHI S., TOYOSHIMA K., AKIYAMA T.;
MATSUMINE A., KOBAYASHI S., TOYOSHIMA K., AKIYAMA T.;
DAP-1, a novel protein that interacts with the guanylate kinase-like
domains of hDLG and PSD-95.";
GENES TO CELLES 7.2(15-244(1997).
EMBL; AB000276; D1024134; -
SEQUENCE 675 AA; 75260 MW; IFFE2AC4 CRC32;
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TAKAMISTA C., SUN J., KITABATAKE A., SOBUE K.;
"Differential expression of isoforms of PSD-95 binding protein (GRAP/SAPAPI) during rat brain development.";
FEBS. LETT. 418 301-304 (1997).
EMBL, AB003594; D1025176; -.
SEQUENCE 692 AA, 76991 MW; CD061633 CRC32;
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Pred. No. 8.55e-01;
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Pred. No. 8.55e-01;
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Pred. No. 8.55e-01;
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01-JAN-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
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SEQUENCE FROM N.A.
MEDLINE; 98089008.
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Pred. No.
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Similarity 85.7%;
6; Conservative
      larity 85.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                          PRELIMINARY;
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01-AUG-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                               01-AUG-1998 (TREMBLREL.
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Matches 6; Conserv
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Best Local Similarity
    Best Local Similarity
Matches 6; Conser
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                                                                  436 EHSSRLQ 442
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                                                                                     1 EHSSKLQ 7
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| EHSSKLQ 7
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061529
061529;
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                                                                                                                                                              01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
PSD-95/SAP90-ASSOCIATED PROTEIN-1.
RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FERINBERISTOL NO.

MEDLINE; 94150718

MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COLLSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULLON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCHUNGRAY A., MORTIMORE B., O'CALLAGIAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SILSTON J.,
THIERRY MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WAIRESTON R.,
WAISON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA; RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 42; DB 11; Length 992;
Pred. No. 8.55e-01;
1; Mismatches 0; Indels
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STRAIN-BRISTOL N2;
WATERSTON R.;
WATERSTON R.Y.
SUBMITTED (NOV-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U80436; G1703564; ...
PFAM; PF00621; RhoGEF; 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DU Z., LE T.;
SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1548 AA; 179071 MW; 63FBFA8A CRC32;
                                                                                                                                                                                                                                                                                                                                                                            37; G1864087; -.
992 AA; 110177 MW; 7D090FD0 CRC32;
                                                                                                    992 AA
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TAKAI Y., TAKEUCHI M., IRIE M., HATA Y.;
J. BIOL. CHEM. 0:0-0(0).
EMBL: U67137; G1864087; --
                                                                                                                                             CREATED)
                                                                                                       PRT;
                                                                                                                                         01-MAY-1997 (TREMBLREL. 03, 01-MAY-1997 (TREMBLREL. 03, 01-AUG-1998 (TREMBLREL. 07,
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similarity 85.7%;
6; Conservative
                                                                                                    PRELIMINARY;
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Matches 6; Conserv
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EHSSKLQ 7
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P97836;
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STEAINN 12;

MEDLINE; 98188103.

STEVEN R., KUBLESSI T.J., ZHENG H., KULKARNI S., MANCILLAS J.,

RUIZ MORALES A., HOGUE C.W.V., PAWSON T., CULOTTI J.;

"UNC-73 activates the Rac GTPase and is required for cell and growth cone migrations in C. elegans.";

CELL 92.785-795 (1998).

EMBL; AF048835; G2944398; -

SEQUENCE 1638 AA; 189071 MW; 83310A21 CRC32;
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MEDLINE; 99189103.
STEATON X;
MEDLINE; 99189103.
STEATON X., KUBISESKI T.J., ZHENG H., KULKARNI S., MANCILLAS J.,
STEATON X, KUBISESKI T.J., ZHENG H., KULKARNI S., MANCILLAS J.,
"UNC-73 activates the Rac GTPase and is required for cell and growth cone migrations in C. elegans.";
CELL 92:795-795(1998).
EMBL: AF048934; G2944396; -...
SEQUENCE 2488 AA; 282876 MW; 40A8CB92 CRC32;
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RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
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RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
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Pred. No. 8.55e-01;
1; Mismatches 0; Indels
                                Indels
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                                                                                                                                                                                                                                                                                                                01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
GUANINE NUCLEOTIDE EXCHANGE FACTOR UNC-73B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
GUANINE NUCLEOTIDE EXCHANGE FACTOR UNC-73A.
. No. 8.55e-01;
Mismatches 0;
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STRAIN-K-12;
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SACTERIA; PF
PSEUDOMONAS.
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P76092
P76092;
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                                                                                                                                                                                                                                                     NĀRCISSUS PSEUDONARCISSUS (DĀFFODIL).
EUKĀRYCVĀ, VIRIDIPLAMYRE; STREPTOPHYTĀ; EMBRYOPHYTĀ; TRACHĒOPHYTĀ;
EUPHYLLOPHYTĒS; SPĒRMĀTOPHYTĀ; MAGNOLIOPHYTĀ; LILIOPSIDĀ; ASPĀRĀGĀLĒS;
AMĀRYLLIDĀCĒĀĒ; NARCISSUS.
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TISSUE-PARACOROLLA;

MEDLINE; 9608151.

NIEVELSTEIN V., VANNEKERCKHOVE J., TADROS M.H., LINTIG J.V.,

NITSCHKE W., BEYER P.;

NITSCHKE W., BEYER P.;

Carotene desaturation is linked to a respiratory redox pathway is

Narcissus pseudonarcissus chromoplast membranes. Involvement of a

3.ADA oxygen-evolving-complex-like protein.";

EUR. J. BIOCHEM. 233:864-872(1995).

EMBL: X78816; A780273;

MENDEL: 11966: NARPS:PSDP:1.

SEQUENCE 265 Aa; 28521 MW; BF1116D6 CRC32;
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Pred. No. 3.23e+00;
2; Mismatches 0; Indels
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Pred. No. 3.23e+00;
3; Mismatches 0; Indels
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"Molecular basis for antigenic variation of a protective strain-specific antigen of Ehrlichia risticii.";
INFECT. IMMUN. 66:3682-3688(1998).
EMBL: AF059673: G3414803; -.
SEQUENCE 849 AA; 93299 MW; BC65E036 CRC32;
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LAST SEQUENCE UPDATE)
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           265 AA
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           PRELIMINARY;
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MEDLINE; 98339868.
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MORITA H., KASAI H., ISONO K.;
"Cloning and characterization of the hrpa gene in the terC region of Escherichia coli that is highly similar to the DEAH family RNA helicase genes of Saccharomyces cerevisiae.";
NUCLEIC ACIDS RES. 23:595-598(1995).
EMBL. DASO81: G1787678;
HYPOTHETICAL PROTEIN
                                                                                                                                   MEDINE; 98115919.
BOGDANOVE A.J., KIM J.F., WEI Z., KOLCHINSKY P., CHARKOWSKI A.O., COLLMEIN A.K., COLLMER A., BERE S.V.;
"HOMOLOGY and functional similarity of an hrp-linked pathogenicity locus, dspEF, of Erwinia amylovora and the avirulence locus avrE of Pseudomonas sylingae pathovar tomato.",
BNGC. NATL. ACAD. SCI. U.S.A. 95:1325-1330(1998).
EMBL; U97505; G2978503; ...
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BLATTNER F.R., PLUNKETT III G., BLOCH C.A., PERNA N.T., BURLAND V., BLATTNER F.R., PLUNKETT III G., BLOCH C.A., RODE C.K., MAYHEW G.F., RILEY M., COLLADO-VIDES J., GLASNER J.D., RODE C.K., MAYHEW G.F., MAU B., SHAO Y., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J., MAU B., SHAO Y.;
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MEDLINE; 92190338.

MOSZER I., GLASER P., DANCHIN A.;

"Multiple IS insertion sequences near the replication terminus in

Escherichia coli K-12.";

BIOCHIMIE 73:1361-1374(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1997 (TREMBLREL. 02, CREATED)
01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
FROM BASES 1472112 TO 1485151
(SECTION 128 OF 400) OF THE COMPLETE GENOME (SECTION 128 OF 400).
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PROTEOBACTERIA; GAMMA SUBDIVISION; PSEUDOMONAS GROUP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of Escherichia coli K-12."; SCIENCE 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40; DB 2; Length 1795
Pred. No. 3.23e+00;
1; Mismatches 0; Indels
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SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                            1795 AA; 195351 MW; 14A8A737 CRC32;
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MEDLINE; 95206938.
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HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI: HOMINIDAE; HOMO.
                Gaps
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SEQUENCE FROM N.A.
MEDLINE; 98389898.
KARKI S., LAMONTE B., HOLZBAUR E.L.F.;
"Characterization of the p22 subunit of dynactin reveals the localization of cytoplasmic dynein and dynactin to the midbody of dividing cells."; 142:1023-1034 (1998).
EMBL; AF082513; G3649657; -.
SEQUENCE 186 AA; 21119 MW; 7B47CEC9 CRC32;
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Best Local Similarity 71.4%; Pred. No. 6.19e+00;
Matches 5; Conservative 2; Mismatches 0; Indels
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075935 PRELIMINARY;
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01-NOV-1998 (TREMBLREL. 0:
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Search completed: Thu Oct 28 11:26:30 1999 Job time: 39 secs.

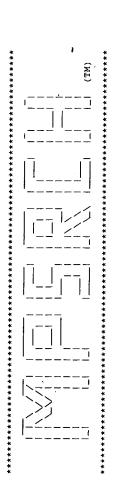
121 EHAARLQ 127

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Oct 28 11:29:02 1999; MasPar time 3.25 Seconds 45.813 Million cell updates/sec Run on:

Tabular output not generated

>US-09-081-707-11 (1-7) from US09081707.pep 49 Description: Perfect Score:

1 QNKISYQ 7 Sequence:

PAM 150 · Gap 15 Scoring table:

170751 seqs, 21266608 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

a-genesed35 Database:

| part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part10 11:part11 12:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 39:part39 35:part39 35:part39 35:part39 35:part39 37:part37 38:part38

Mean 14.672; Variance 35.519; scale 0.413 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Pred. No.	VSA1 1.11e+01				. [ - 0	. [ - 0   0	. 1 - 01 01 01	. 1 - 01 01 01 01	. 1 < 01 01 01 01 01 01	. 12 01 01 01 01 01 01	. 1 < 0   0   0   0   0   0   0   0	ant sant sant sant sant sant sant sant s	aant sant sant sant sant sant sant sant	aant saant s	aant gaant gaak
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ΙΩ	W51096	W33439	R89602	R89612	W33449	W33546	W33435	R89598	R89712	R89599	R89718	W33552	W33488	W33448	
DB	32	56	17	17	56	56	56	17	17	17	17	56	56	26	
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& Query Match	100.0	87.8	87.8	85.7	85.7	85.7	85.7	85.7	85.7	85.7	85.7	85.7	85.7	85.7	
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Seguence

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#### ALIGNMENTS

Claim 3; Fig 2C; 39pp; English.

Claim 3: Fig 2C; 39pp; English.

This is the full-length variable surface antigen VSAI protein of Enlichia canis. Its amino acid sequence was deduced from open reading frame (ORF) 1 of a genomic locus (see VO7180) of E. canis that was obtained on the basis of homology to the major antigenic protein MAPI (see W51088) of Cowdria ruminantium. This genomic locus included 2 ORFs encoding similar, but non-identical proteins (see W51096-97). A claimed composition comprises a nucleic acid see W51076-82) encoding a polypeptide (see W51088-99) that elicits a protective immune response against a rickettsial pathogen. The nucleic acid is used, in human or veterinary medicine, in vaccines to protect against Rickettsia, Ehrlichia, Anaplasma and Cowdria species. The Ehrlichia antigenic polypeptides can be used diagnostically to detect antibodies associated with Ehrlichia WPI: 98-251232/22. N-PSDB: V07180. Composition containing nucleic acid encoding rickettsial antigen -useful for, e.g. stimulating protective immune response in humans or W51096; 14-SEP-1998 (first entry) Ehrlichia canis VSA1 protein (partial sequence). MAP1 homologue; variable surface antigen; VSA1; rickettsia; \$2-APR-1998.) 17-6cT-1992. U19044. 17-0CT-1996. US-733230. (UYE.) UNIV FLORIDA. Barbet AF, Burridge MJ, Ganta RR, Mahan SM, McGuire TC, Nyika A, Rurangirwa FR; 1..25
/note= "putative signal peptide" Location/Qualifiers .T 1 W51096 standard; Protein; 287 AA. Ehrlichia canis. 409816554-A DNA vaccine Peptide SULPHONE SERVICE SERVI a

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  While Y-2229/A-220.

Oligopeptide(s) recognised and cleaved by free prostate specific antigen - useful in assays for active antigen, and in antigen - useful in assays for active antigen, and in proligopeptide-fug conjugates for prostatic cancer treatment bisclosure; Page 81; 192pp; English.

The present sequence is a novel oligopeptide that is recognised and concern treatment is an alor sperm entrapping gel protein. PSA, which has designed based on the sequences surrounding the PSA cleavage sites of semenogelin 1, a major sperm entrapping gel protein. PSA, which has confunctypsin-like specificity is responsible for dissolution of the gel structure formed at ejaculation by proteolysis of the major gel proteins (Semenogelin I and II, and fibronectin). Liquefaction of the ejaculate companies of psA are useful for monitoring treatment of adenocarcinoma measurements of PSA are useful for monitoring treatment of adenocarcinoma of the prostate. Prostate metastases are also known to secrete immunojdically reactive PSA since serum PSA is detectable at high levels in prostatectomised patients showing widespread metastatic prostate concer. Cytotoxic compounds that could be activated by the proteolytic cancer. Cytotoxic compounds that could be activated by the proteolytic of the PSA secreting energiases. Conjugates of cytotoxic compounds and this oligopeptide are useful in treatment of prostate cancer. The oligopeptide can also be useful in a quantitative assay for enzymatically activated by the proteolyte are useful in a quantitative assay for enzymatically activated by the proteolyte are useful in a quantitative assay for enzymatically activated by the proteolyte are useful and activated by the proteolyte are useful in a quantitative assay for enzymatically activated by the proteolyte are useful in a quantitative assay for enzymatically activate cancer.
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                                                     Gaps
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Oligopeptide 19 cleaved by free prostate specific antigen.
Oligopeptide, proteolytic cleavage, prostate specific antigen;
Oligopeptide, proteolytic cleavage, prostate specific antigen; PSA;
cleavage site; Semenogelin I; chymotrypsin-like; serum PSA;
adenocarcinoma; prostate metastasses; prostate cancer; treatment;
detection; cytotoxic conjugate; activation; quantitative assay.
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Length 287;
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Pred. No. 7.10e+01;
1; Mismatches 0; Indels
                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Defeo-Jones D, Feng D, Garsky VM, Jones RE, Oliff AI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "PSA specific cleavage site"
Score 49; DB 32; Le
Pred. No. 1.11e+01;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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R89602 standard; peptide; 17 AA.
                                                                                                                                                                                                                                          JI 2
W33439 standard; Peptide; 17 AA.
W33439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 87.8%;
Best Local Similarity 85.7%;
Matches 6; Conservative
Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-540412.
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02-OCT-1996; U15713.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 97-225974/20.
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                                                                                                           214 qnkisyg 220
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                                                                                                                                                           1 QNKISYQ 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
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                                                                                                                                                                                                                                             RESULT
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WITH 96-07725/08.

WITH 96-07725/08.

WITH 96-07725/08.

WE peptide substrates cleaved by prostate-specific antigen - also cytotoxic conjugates for treating prostate cancer, and assay for determination of PSA activity.

Bisclosure: Page 60: 142pp; English.

Human semenogelin I (ASI) is one of the major proteins, including his including the sperm entrapping gel formed at cation of prostate specific antigen (PSA), a protease with chymotrypsin like specific antigen (PSA), a protease with chymotrypsin like specificity, which proteolyses the above major proteins. New substrates, including the present peptide, cleaved in assays to determine the proteolytic activity of free PSA in a sample, and to identify cpds. which inhibit the proteolytic activity of PSA, they may also be conjugated, via a covalent bond or prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New peptide substrates cleaved by prostate-specific antigen - also cytotoxic conjugates for treating prostate cancer, and assay for determination of PSA activity.

S claim 6: Page 64; 142pp; English.

C laim 6: Page 64; 142pp; English.

C hSII and fibronectin, in the sperm entrapping gel formed at ejaculation. This gel structure undergoes dissolution via the action of prostate specific antigen (PSA), a protease with action of prostate specific antigen (PSA), a protease with proteins. New substrates, including the present peptide, cleaved by PSA, i.e. peptides contg. a hSI PSA cleavage site, can be used in assays to determine the proteolytic activity of FSA, they may also be conjugated, via a covalent bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; semenogelin I; sperm entrapping gel; ejaculation; protease; gel structure; dissolution; prostate specific antigen; proteolysis; chymotrypsin like specificity; peptide substrate; cleavage site; assay; determination; proteolytic activity; identification; inhibitor; cytotoxic agent; conjugated; treatment; prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-SEP-1996 (first entry)
Prostate specific antigen, semenogelin derived, cleavage substrate.
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                                                                                                                                                      Garsky VM, Jones RE, Oliff AI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Garsky VM, Jones RE, Oliff AI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R89612 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.8%;
07-JUN-1995; U08156.
28-JUN-1994; US-267092.
15-MAR-1995; US-404833.
(MEXI ) MERCK & CO INC.
DeFeo-Jones D, Feng D, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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DeFeo-Jones D, Feng D,
WPI; 96-077275/08.
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07-JUN-1995; UO8156.
28-JUN-1994; US-267092.
15-MAR-1995; US-404833.
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10-APR-1997.
02-OCT-1996; U15713.
06-OCT-1995; US-540412.
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2 NKISYQ 7
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                                                                                                                       Cleavage_site
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                                                                                                                                                                                            10-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           active PSA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                           Synthetic.
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Matches
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    PT Oligopeptide(s) recognised and cleaved by free prostate specific antigen - useful in assays for active antigen, and in oligopeptide-fug conjugates for prostatic cancer treatment claim 6; Page 162; 192pp; Branish.

Conforting of the sequences surrounding the pSA cleavage sites of proteolytically cleaved by free prostate specific antigen (PSA). It was designed based on the sequences surrounding the PSA cleavage sites of Semenogelin I, a major sperm entrapping gel protein. PSA, which has chymotrypsin-like specificity is responsible for dissolution of the gel structure formed at ejaculation by proteolysis of the major gel proteins (Semenogelin I and II, and fibronectin). Liquefaction of the ejaculate classes progressively motile spermatozoa. PSA complexed to alpha 1-antichymotrypsin is the predominant form of serum PSA. Serum measurements of PSA are useful for monitoring treatment of adenocarcinoma of the prostate. Prostate metastases are also known to secrete immunologically reactive PSA since serum PSA is detectable at high levels in prostatectomised patients showing widespread metastatic prostate cancer. Cytoroxic compounds that could be activated by the proteolytic cancer contrivity of PSA should also be prostate cell specific as well as specific activity of PSA should also be prostate cell specific as well as specific activity of PSA should also be prostate cell specific as well as specific activity of PSA should are useful in treatment of prostate cancer. The coligopeptide can also be used in a quantitative assay for enzymatically
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                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                    77-MAR.1998 (first entry)
011gopeptide 29 cleaved by free prostate specific antigen.
011gopeptide, protecolytic cleavage; prostate specific antigen; PSA;
011gopeptide, protecolytic cleavage; prostate specific antigen; PSA;
cleavage site; Semenogelin I; chymotrypsin-like; serum PSA;
adenocarcinoma; prostate metastases; prostate cancer; treatment;
detection; cytotoxic conjugate; activation; quantitative assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Oligopeptide 126 based on Semenogelin I cleavage site.
Oligopeptide; proteolytic cleavage; prostate specific antigen; PSA;
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  to a cytotoxic agent and used to treat
                                                                                Score 42; DB 17; Length Pred. No. 9.60e+01;
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Pred. No. 9.60e+01;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "PSA specific cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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W33546 standard; Peptide; 8 AA.
W33546;
                                                                                                                                                                                                                                                                                                     .r 5
W33449 standard; Peptide; 7 AA.
W33449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%;
Matches 6; Conservative
                                                                                          Query Match 85.7%;
Best Local Similarity 100.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-APR-1997.
02-OCT-1996; U15713.
06-OCT-1995; US-540412.
(MERI ) MERCK & CO INC.
or peptide linker,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 97-225974/20.
                                              7 AA;
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                        prostate cancer
Sequence 7 AA
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2 NKISYQ 7
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PT 01190peptide(s) recognised and cleaved by free prostate specific antigoner useful in assays for active antigen, and in antigen useful in assays for active antigen, and in antigen (by 192p). Brailsh.

Claim 3: Page 160, 192pp; English.

Claim 3: Page 160, 192pp; English.

Consequences surrounding the prostate specific antigen (PSA) cleavage sites of Semenogelin I, a major sperm entrapping gel protein. PSA, which has constructe formed at ejaculation by proteolysis of the major gel proteins of Semenogelin I and II, and fibronectin). Liquefaction of the gel structure formed at ejaculation by proteolysis of the major gel proteins of semenogelin I and II, and fibronectin). Liquefaction of the ejaculate concerns of a lantichymotrypsin is the predominant form of serum PSA. Serum massurements of PSA are useful for monitoring treatment of adenocarcinoma of the prostate. Prostate metastases are also known to secrete immunologically reactive PSA since serum PSA is detectable at high levels in prostatectomised patients showing widespread metastatic prostate cancer. Cytotoxic compounds that could be activated by the proteolytic activity of PSA secreting prostate metastases. Conjugates of cytotoxic compounds and this oligopeptide are useful in a quantitative assay for enzymatically are actived by the prostate collapperide can also be used in a quantitative assay for enzymatically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "this Ser is optionally attached via a peptide
bond to the 3'-amino group on the sugar ring of
doxorubicin, alternatively it is optionally
amidated when the peptide is N-terminally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Oligopeptide 15 cleaved by free prostate specific antigen.
Oligopeptide, proceolytic cleavage; prostate specific antigen;
Oligopeptide, proceolytic cleavage; prostate specific antigen; PSA;
cleavage site; Semenogelin I; chymotrypsin-like; serum PSA;
adenocarcinoma; prostate metastases; prostate cancer; treatment;
detection; cytotoxic conjugate; activation; quantitative assay.
cleavage site; Semenogelin I; chymotrypsin-like; serum PSA; adenocarcinoma; prostate metastases; prostate cancer; treatment; detection; cytotoxic conjugate; activation; quantitative assay.
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Pred. No. 9.60e+01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DeFeo-Jones D, Feng D, Garsky VM, Jones RE, Oliff AI;
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                                                                                                                                                                                                                                                              /note= "PSA specific cleavage site"
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Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MERI ) MERCK & CO INC.
                                                                                                                                                                                                                                                                                                                                                                                                    02-OCT-1996; U15713.
06-OCT-1995; US-540412.
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ejaculation. This gel structure undergoes dissolution via the
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2 NKISYQ 7
                                                                                                                                                                                                                                                                                                                    2 NKISYQ 7
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                                     Oligopeptide(s) recognised and cleaved by free prostate specific antigen - useful in assays for active antigen, and in antigen - useful in assays for active antigen, and in coligopeptide-fung conjugates for prostatic cancer treatment Claim 3 and 7 and 17: Page 160: 193pp: English.

Claim 3 and 7 and 17: Page 160: 193pp: English.

CC The present sequence is a novel oligopeptide that is recognised and conflict of sequences surrounding the PSA cleavage sites of Semenogelin I, a major sperm entrapping gel protein. PSA, which has of Semenogelin I, and or sperm entrapping gel protein. PSA, which has confortable in and II, and fibronectin). Liquefaction of the gel confortable in and II, and fibronectin). Liquefaction of the gel confortable in and II, and fibronectin). Liquefaction of the gel proteins of samenogelin I and II, and fibronectin). Liquefaction of the gel proteins of samenogelin I and II, and fibronectin). Liquefaction of the gel proteins of samenogelin I and indipersorate spermatozoa. PSA complexed to alpha 1-antichymotrypsin is the predominant form of serum PSA. Serum measurements of PSA are useful for monitoring treatment of adenocarcinoma of the prostate. Prostate metastases are also known to secrete immunologically reactive PSA should also be prostate cell specific as well as specific control and this oligopeptide are useful in treatment of prostate cancer. The collopopeptide are useful in treatment of prostate cancer. The collopopeptide and also be used in a quantitative assay for enzymatically active PSA. In a study of cleavage affinity, the TFA salt of this peptide the next and a disputed for the propertion of an also contained and a certained and experience of dispeted with enzymatically active PSA. After four hours 30 per cent of the hourshild also be asset.
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Claim 3; Page 58: 142pp: English.
Human semenogelin I (KIS) is one of the major proteins, including hSI, and fibronectin, in the sperm entrapping gel formed at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 42; DB 26; Length 8;
Pred. No. 9.60e+01;
0; Mismatches 0; Indels
             Feng D, Garsky VM, Jones RE, Oliff AI;
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R89598 standard; peptide; 8 AA.
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11-JAN-1996.
07-JUN-1995; U08156.
28-JUN-1994; US-267092.
15-MAR-1995; US-404833.
(MERI ) MERCK & CO INC.
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Best Local Similarity 100.0%;
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(MERI ) MERCK & CO INC
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WPI: 96-077275/08.
             DeFeo-Jones D, Fen
WPI; 97-225974/20.
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2 NKISYQ 7
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Tototoxic conjugates for treating prostate cancer, and assay for determination of PSA activity

Claim 3: Page 108: 142pp: English.

Human semenogelin I (hSI) is one of the major proteins, including cancer and fibronectin. In the sperme entrapping get formed at cartion of prostate specific antigen (PSA), a protease with action of prostate specific antigen (PSA), a protease with action of prostate specificing, which proteologss the above major proteins. New substrates, including the present peptide, cleaved by PSA, i.e. peptides contg. a hSI PSA cleavage site, can be used in assays to determine the proteolytic activity of free PSA in a sample, and to identify of so, which inhibit the proteolytic activity of pSA, they may also be conjugated, via a covalent bond or peptide linker, to a cytotoxic agent and used to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prostate specific antigen, semenogelin derived, cleavage substrate. Human; semenogelin I; sperm entrapping gel; ejaculation; protease; gel structure; dissolution; prostate specific antigen; proteolysis; chymotrypsin like specificity; peptide substrate; cleavage site; assay; determination; proteolytic activity; identification; inhibitor; cytotoxic agent; conjugated; treatment; prostate cancer.
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chymotrypsin like specific antigen (PSA), a protease with chymotrypsin like specificantigen (PSA), a protease with chymotrypsin like specificatity, which proteolyses the above major proteins. New substrates, including the present peptide, cleaved by PSA, i.e. peptides contg a hSI PSA cleavage site, can be used in assays to determine the proteolytic activity of free PSA in a sample, and to identify cpds, which inhibit the proteolytic activity of PSA, they may also be conjugated, via a covalent bond or peptide linker, to a cytotoxic agent and used to treat the present peptide cleaved by YORK PSA after 4 hrs. was 30 % acylated and amidated.
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Pred. No. 9.60e+01;
0; Mismatches 0; Indels
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Pred. No. 9.60e+01;
0; Mismatches 0;
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Best Local Similarity 100.0%;
Matches 6; Conservative
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Best Local Similarity 100.0%;
Matches 6; Conservative
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DeFeo-Jones D, Feng D,
WPI; 96-077275/08.
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07-JUN-1995; UO8156.
28-JUN-1994; US-267092.
15-MAR-1995; US-404833.
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T determination of psA activity

Glaim 3: Page 58: 142pp: English

Human semenogelin I (hSI) is one of the major proteins, including hSI and fibronectin, in the sperm entrapping gel formed at ejaculation. This gel structure undergoes dissolution via the action of prostate specificity, which proteolyses the above major chymotrypsin like specificity, which proteolyses the above major chymotrypsin like specificity, which proteolyses the above major chymotrypsin like specificity, which proteolyses the above major by PSA, i.e. peptides contg. a hSI PSA cleavage site, can be used in assays to determine the proteolytic activity of free PSA in a sample, and to identify cpds. which inhibit the proteolytic activity of PSA, they may also be conjugated, via a covalent bond or peptide linker, to a cytotoxic agent and used to treat proteoly present peptide cleaved by YORK PSA after 4 hrs. was 55 %.
                                                                                Prostate specific antign, semenogelin derived, cleavage substrate. Human; semenogelin I; sperm entrapping gel; ejaculation; protease; gel structure; dissolution; prostate specific antigen; proteolysis; chymotrypsin like specificity; peptide substrate; cleavage site; assay; determination; proteolytic activity; identification; inhibitor; cytotoxic agent; conjugated; treatment; prostate cancer.
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                       standard; peptide; 9 AA
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DeFeo-Jones D, Feng D,
WPI; 96-077275/08.
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07-JUN-1995; U08156.
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DeFeo-Jones D, Feng D,
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The presult sequences is a nover consequence surrounding the prostate specific antigen (PSA) cleavage sites of Semenogelin I, a major sperm entrapping gel protein. PSA, which has conventive sortificity is responsible for dissolution of the gel structure formed at ejaculation by proteolysis of the major gel proteins of the major gel proteins structure formed at ejaculation by proteolysis of the major gel proteins (Semenogelin I and II, and fibronectin). Liquefaction of the ejaculate of the alpha I-antichymotrypsin is the predominant form of serum PSA. Serum measurements of PSA are useful for monitoring treatment of adenocarcinoma of the prostate. Prostate metastases are also known to secrete immunologically reactive PSA since serum PSA is detectable at high levels in prostatectomised patients showing widespread metastatic prostate cancer. Cytotoxic compounds that could be activated by the proteolytic or cancer. Cytotoxic compounds that could be activated by the proteolytic for PSA secreting prostate metastases. Conjugates of cytotoxic compounds and this oligopeptide are useful in treatment of prostate cancer. The oligopeptide can also be used in a quantitative assay for enzymatically
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                                                                                                                              Claim 4; Page 111, 142pp; English.

Claim 4; Page 111, 142pp; English.

C Human semenogelin I (hSI) is one of the major proteins, including hSII and fibronectin, in the sperm entrapping gel formed at ejaculation. This gel structure undergoes dissolution via the action of prostate specific antigen (PSA), a protease with chymotrypsin like specificanty, which proteolyses the above major proteins. New substrates, including the present peptide, cleaved in assays to determine the proteolytic activity of free PSA in a sample, and to identify codes, which inhibit the proteolytic activity of PSA, they may also be conjugated, via a covalent bond or peptide linker, to a cytotoxic agent and used to treat
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Claim 4; Page 161; 192pp; English.
The present sequence is a novel oligopeptide designed based on the
New peptide substrates cleaved by prostate-specific antigen - algoritotoxic conjugates for treating prostate cancer, and assay for determination of PSA activity
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Pred. No. 9.60e+01;
0; Mismatches 0; Indels
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WPI; 97-225974/20.
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Best Local Similarity 100.0%;
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02-OCT-1996; U15713.
06-OCT-1995; US-540412.
(MERI ) MERCK & CO INC.
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2 NKISYO 7
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Length 9;

DB 26;

85.7%; Score 42;

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                  Synthetic.
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The present sequence is a novel oligopeptide that is recognised and protein protein lyse agence is a novel oligopeptide that is recognised and protein protein protein protein PSA, which has designed based on the sequences surrounding the PSA cleavage sites of semenogalin I, a major specificity is responsible for dissolution of the gel structure formed at ejaculation by proteolysis of the major gel proteins (Semenogalin I and II, and fibronectin). Liquefaction of the ejaculate calcases progressively motile spermatozoa. PSA complexed to alpha I-antichymotrypsin is the predominant form of serum PSA. Serum measurements of PSA are useful for monitoring treatment of adenocarcinoma of the prostate. Prostate metastases are also known to secrete immunologically reactive PSA since serum PSA is detectable at high levels in prostatectomised patients showing widespread metastatic prostate cancer. Cytotoxic compounds that could be activated by the proteolytic activity of PSA should also be prostate cell specific as well as specific for PSA secreting prostate metastases. Conjugates of cytotoxic compounds and this oligopeptide are useful in treatment of prostate cancer. The oligopeptide are useful in treatment of prostate cancer. The oligopeptide was digested with enzymatically active PSA. After 4 hours 39 per cent of the peptide was cleaved.
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                                            Gaps
                                                                                                                                                                                                                                                                  27-MAR-1998 (first entry)
Oligopeptide 68 cleaved by free prostate specific antigen.
Oligopeptide, proteolytic cleavage, prostate specific antigen; PSA, cleavage site; Semenogelin I; chymotrypsin-like; serum PSA, adenocarcinoma; prostate metastases; prostate cancer; treatment; detection; cytotoxic conjugate; activation; quantitative assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W33448 standard; Peptide; 10 AA.
W33448 W3348;
W33448;
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Pred. No. 9.60e+01;
0; Mismatches 0; Indels
                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Feng D, Garsky VM, Jones RE, Oliff AI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "PSA specific cleavage site"
Pred. No. 9.60e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                     T 13
W33488 standard; Peptide; 9 AA.
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Best Local Similarity 100.0%;
Matches 6; Conservative
                  Best Local Similarity 100.0%;
                                            Conservative
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02-OCT-1996; U15713.
06-OCT-1995; US-540412.
(MERI ) MERCK & CO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97-225974/20.
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2 NKISYQ 7
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                                                                                                           Cleavage_site
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                                                                                    nkisyq
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with yor reason, we will be a seays for active antigen, and in an antigen useful in assays for active antigen, and in an antigen useful in assays for active antigen, and in antigen useful in assays for active antigen, and in antigen to ligopeptide-drug conjudates for prostatic cancer treatment claim 6; Page 162; 192pp; English.

Claim 6; Page 162; 192pp; English.

Claim 6; Page 162; 192pp; English.

CC proteolytically cleaved by free prostate specific antigen (PsA). It was designed based on the sequences surrounding the PsA cleavage sites of commorphin 1, a major sperm entrapping gel protein. PsA, which has composed in 1, and proposed protein protein protein of the gel criman and II, and fibronectin). Liquefaction of the ejaculate composes progressively metile spermatozoa. PsA complexed to alpha 1-antichymotrypsin is the predominant form of serum PsA. Serum measurements of PsA are useful for monitoring treatment of adenocarcinoma of the prostate. Prostate metastases are also known to secrete immunologically reactive PsA since serum PsA is detectable at high levels in prostatectomised patients showing widespread metastatic prostate compounds that could be activated by the proteolytic cancer, the prostate metastases. Conjugates of cyctoxic compounds and this oligopeptide are useful in treatment of prostate cancer. The concerned on a quantitative assay for enzymatically concerned and this oligopeptide and also be used in a quantitative assay for enzymatically concerned and the concerned in a quantitative assay for enzymatically concerned to the concerned of a concerned to the concerned to conce
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bond to the 3'-amino group on the sugar ring of
doxorubicin"
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27-MAR-1998 (first entry)
Oligopeptide 9 cleaved by free prostate specific antigen.
Oligopeptide; proteolytic cleavage; prostate specific antigen; PSA;
cleavage site; Semenogelin I; chymotrypsin-like; serum PSA;
adenocarcinoma; prostate metastases; prostate cancer; treatment;
detection; cytotoxic conjugate; activation; quantitative assay.
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                                                                                                                                                                                                                                                                                                                                           (MERI ) MERCK & CO INC.
DeFeo-Jones D, Feng D, Garsky VM, Jones RE, Oliff AI;
                                                                                           /note= "PSA specific cleavage site"
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Location/Qualifiers
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Best Local Similarity 100.0%;
Matches 6; Conservative
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02-OCT-1996; U15713.
06-OCT-1995; US-540412.
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06-OCT-1995; US-540412.
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DeFeo-Jones D, Feng D,
WPI; 97-225974/20.
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The present sequence is a novel oligopeptide that is recognised and proteolytically cleaved by free prostate specific antigen (PSA). It was casing a based based on the sequences surrounding the PSA cleavage sites of Semenogelin I, a major sperm entrapping gel protein. PSA, which has consequent I, a major sperm entrapping gel protein. PSA, which the gel structure formed at ejaculation by proteolysis of the major gel proteins CS semenogelin I and II, and fibronectin). Liquefaction of the ejaculate creleases progressively motile spermatozoa. PSA complexed to alpha I-antichymotrypsin is the predominant form of serum PSA. Serum measurements of PSA are useful for monitoring treatment of adenocarcinoma of the prostate. Prostate metastases are also known to secrete immunologically reactive PSA since serum PSA is detectable at high levels of prostatectomised patients showing widespread metastatic prostate cancer. Cytotoxic compounds that could be activated by the proteolytic activity of PSA should also be prostate cell specific as well as specific of or PSA secreting prostate metastases. Conjugates of cytotoxic compounds and this oligopeptide are useful in treatment of prostate cancer. The citypeptide can also be used in a quantitative assay for enzymatically contine PSA. In a study of cleavage affinity, the TFA salt of this peptide was cleaved.

Sequence 10 AA;
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Ouery Match 85.7%; Score 42; DB 26; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.60e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps
Db 1 nkisyq 6
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Search completed: Thu Oct 28 11:29:19 1999 Job time: 17 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm

MPsrch\_pp

Thu Oct 28 11:29:36 1999; MasPar time 2.95 Seconds 95.143 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-081-707-11 (1-7) from US09081707.pep 49

1 QNKISYQ 7 Description: Perfect Score: Sequence: 122810 seqs, 40068593 residues Searched:

PAM 150 Gap 15

Scoring table:

Post-processing: Minimum Match 0% Listing first 45 summaries

pir60 Database:

Mean 20.354; Variance 20.844; scale 0.976 1:pirl 2:pir2 3:pir3 4:pir4 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Pred. No.	2.00e-01	2.11e+00	2.11e+00	1.13e+01	1.13e+01	1.93e+01	1.93e+01	1.93e+01	1.93e+01	3.28e+01	3.28e+01	3.28e+01	5.51e+01	5.51e+01	5.51e+01								
Description	28k surface antiqen 1	semenogelin II precur	carbonic anhydrase II	hypothetical protein	semenogelin I precurs	hypothetical protein,	early E3B 14K protein	factor H - bovine (fr	beta-qlucosidase (EC	early E3B 15.3K prote	E3 gene encoding hypo	hypothetical protein,	hypothetical 16K prot	probable yop transloc	fimbrial adhesin F17-	HE65 protein - Autogr	DNA topoisomerase (EC	nonstructural protein	type III restriction	type III restriction	flagellar basal-body	group 3 Lea protein M	hypothetical protein
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ID	JE0220	A43412	147228	A64214	WIHUB	<b>S52806</b>	ERAD29	865551	GLHQ	ERAD74	JC4773	C37476	S56414	H71497	A42359	I49834	E64213	MNXR3D	A64710	E71810	JG0019	S41387	B71664
DB	~	~	0	~		~	Н	~	Н	Н	~	7	~	~	7	7	~	Н	7	~	~	~	7
Length	287	582	704	145	462	136	136	699	825	135	135	135	142	326	344	553	709	719	296	696	129	221	248
Query	100.0	91.8	91.8	85.7	85.7	83.7	83.7	83.7	83.7	81.6	81.6	81.6	81.6	81.6	81.6	81.6	81.6	81.6	81.6	81.6	9.62	9.64	79.6
Score	49	45	45	42	42	41	41	41	41	40	40	40	40	40	40	40	40	40	40	40	39	33	39
Result No.	-	2	m	4	S	9	7	00	O	10	11	12	13	14	15	16	17	18	19	20	21	22	23

##molecule\_type DNA ##residues 1-582 ##label ULV

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Gaps

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Score 49; DB 2; Length 287; Pred. No. 2.00e-01; 0; Mismatches 0; Indels

Query Match 100.0%; Best Local Similarity 100.0%; Matches 7; Conservative

SUMMARY

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##rcross-references GB:AF062762 ##cross-references GB:AF062762 RY #length 287 #molecular-weight 32014 #checksum 463

#text_change ahan, S.M.; 36-643 ce antigen gene
hia canis 21-Aug-1998 rbet, A.F.; M (1998) 247:6 a 28kDa surfa
completers of the completers o
JE0220 #type c 28k surface antige #formal_name Ehrli 17-Mar_1998 #seque 17-Mar_1999 JE0220 JE0220 JE0220 Buridge, M.J.; Buridge, M.J.; Buridge, M.J.; Molecular characte family of the tr Toes MUID:98321180 JE0220
RESULT 1 JE0220 TITLE 28k surfac DATE #formal_na DATE #formal_na 17-Mar-1 JE0220 17-Mar-1 JE0220 REFERENCE JE0216 #authors Reddy, G.R #ijournal Biochem. B #title Biochem. B #title Molecular family o #cross-references MUID:9 #accession JE0220 #accession JE0220 #accession JE0220

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Best Local Similarity
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                                                                                 Lilja, H.; Abrahamsson, P.A.; Lundwall, A. J. Elol. Chem. (1989) 264:1894-1900 Semenogelin, the predominant protein in human semen. Primary structure and identification of closely related proteins in the male accessory sex glands and on the spermatozoa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           simultaneously with the sequence with accession number $29155 (see entry WTHUB); as a secondary sequence, it should be considered less than fully reliable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##molecule_type protein
##residues 105-107,'K',109-111;113-122;260-269;280-283 ##label KIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eur. J. Biochem. (1996) 238:48-53
Solation and characterization of the major gel proteins in
human semen, semenogelin I and semenogelin II.
S68762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Malm, J.; Hellman, J.; Magnusson, H.; Laurell, C.B.; Lilja,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #domain signal sequence #status predicted #label SIGN
#product semenogelin II #status predicted #label MATN
#binding_site carbohydrate (Asn) (covalent) #status
predicted
#length 582 #molecular-weight 65444 #checksum 9704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##molecule_type protein
##residues 390,'E',392-396,'E',398-400,'EW',403-405,'C',407,'DE'
##residues ##label SCH
##note this report is of a secondary sequence determined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           duplication; glycoprotein; semen; seminal vesicle; tandem
##cross-references GB:M81651; NID:g307417; PID:g307418
##note sequence extracted from NCBI backbone (NCBIN:112887,
NCBIP:112889)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schneider, K.; Kausler, W.; Tripier, D.; Jouvenal, K.;
                                                                                                                                                                                                                                                                                          #authors Lilja, H.; Lundwall, A.
#journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:4559-4563
#title Molecular cloning of epididymal and seminal vesicular transcripts encoding a semenogelin related protein.
#cross-references MUID:92262479
#accession A45295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spiteller, G.
Biol. Chem. Hoppe-Seyler (1989) 370:353-356
Isolation and structure determination of two peptides
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                                                                                                                                                                                                                                nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##molecule_type protein
##residues 420-421,'G',423-423 ##label MAL
                                                                                                                                                                                                                                                                      214-278,'Y',280-281 ##label LIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          occurring in human seminal plasma. $29156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##cross-references GDB:132657; OMIM:182141
#map_position 20q12-20q13.1
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##residues 3-582 ##label LI2
##cross-references GB:M81652
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                                                                                                                                                                                       #cross-references MUID:89109215
#accession B31489
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##residues 214-2
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#authors Roush, E.D.; Fierke, C.A.
#journal Biochemistry (1992) 31:12536-12542
#title Purification and characterization of a carbonic anhydrase II inhibitor from porcine plasma.
#cross-references MUID:93099129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #authors

Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton
R.A.; Fleischmann, R.D.; Bult, C.J.; Kerlavage, A.R.;
Sutton, G.; Kelley, J.M.; Fritchman, J.L.; Weidaman, J.F.;
Small, K.V.; Sandusky, M.; Futhrmann, J.; Nguyen, D.;
Utterback, T.R.; Sandek, D.M.; Phillips, C.A.; Merrick,
J.M.; Tomb, J.F.; Dougherty, B.A.; Bott, K.F.; Hu, P.C.;
Lucier, T.S.; Peterson, S.N.; Smith, H.O.; Hutchison III,
C.A.; Venter, J.C.
#journal Science (1995) 270:397-403
#title
#cross-references MulD:96026346
#accession A64214
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hypothetical protein homolog MG127 - Mycoplasma genitalium
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#formal_name Sus scrofa domestica #common_name domestic
21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change
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10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change
09-Apr-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *superfamily transferrin; transferrin repeat homology duplication
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Pred. No. 2.11e+00;
2; Mismatches 0; Indels
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Pred. No. 2.11e+00;
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                         larity 85.7%;
Conservative
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Similarity 71.4%;
5; Conservative
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#authors Lilja, H.; Abrahamsson, P.A.; Lundwall, A.
#journal Jaiol. Chem. (1989) 264:1894-1900
#title Semenogelin, the predominant protein in human semen. Primary structure and identification of closely related proteins in the male accessory sex glands and on the spermatozoa.
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FEBS Lett. (1985) 182:181-184
Amino acid sequence of the predominant basic protein in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #title Gene structure of semenogelin I and II. The predominant proteins in human semen are encoded by two homologous genes on chromosome 20.
#cross-references MUID:92388176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ulvsback, M.; Lazure, C.; Lilja, H.; Spurr, N.K.; Rao, V.V.; Loffler, C.; Hansmann, I.; Lundwall, A.
J. Biol. Chem. (1992) 267:18080-18084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         this sequence represents a naturally occurring fragment
from proteolytic cleavage of semenogelin during
liquefaction of semen
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this sequence represents the amino end of a naturally
occurring fragment from proteolytic cleavage of
semenogelin during liquefaction of semen
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Manjunath, P.; Schiller, P.W.; Yamashiro, D.; Li, C.H.
                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                            #formal_name #common_name man
04-Dec-1986 #sequence_revision 03-Oct-1995 #text_change
26-Feb-1999
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Biol. Chem. Hoppe-Seyler (1989) 370:353-356
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                                                                                  Score 42; DB 2; Length 145;
Pred. No. 1.13e+01;
0; Mismatches 0; Indels
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##residues 1-78,'T',80-422,'K',424-462 ##label LIL
##cross-references GB:J04440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #accession B43412
##molecule_type DNA
##residues 1-462 ##label ULV
##cross-references GB:M81650; NID:g307416; PID:g487420
                      #superfamily hypothetical protein yjbD #length 145 #molecular-weight 16565
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seminal basic protein
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#cross-references MUID:85127550
#accession A91335
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Best Local Similarity 100.0%;
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#genetic_code SGC3
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been proven the andated tripeptide Glp-Glu-Pro-NH2 (where Glp is pyroglutamic acid) is present in human semen; although the sequence reported here is consistent with an amino-terminally extended form derived from semenogelin, the sequence is followed in semenogelin by Trp, which. (unlike Gly) probably cannot become the source of an amide moiety; the authors conclude the peptide must be derived from a closely related protein
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##molecule_type protein
##residues 373-397 ##label KHA
##residues the authors' suggestion that this peptide is amidated is
##note consistent with radioimmunoassay results but has not
#journal Science (1984) 223:1199-1202
#title Isolation, structure, and synthesis of a human seminal plasma peptide with inhibin-like activity.
#cross-references MUID:84146751
#accession A43500
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Eur. J. Biochem. (1993) 212:35-40
Isolation and identification of N-terminally extended forms of 5-oxoprolylglutamylprolinamide (Glp-Glu-Pro-NH(2)), a thyrotropin-releasing-hormone(TRH)-like peptide present in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           this sequence represents a naturally occurring fragment
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##residues
49-50,'G',52-53 ##label MAL
##residues
Apundant protein from seminal vesicle secretions maintains
gel-like environment for the sperm cells. At ejaculation,
kallikrain-like enaymes in prostatic secretions cleave this
protein, resulting in liquefaction of the seminal gel and
allowing increased sperm motility.
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##molecule_type protein
##residues 108-138 ##label RAM
##note this sequence represents a naturally occurring fra
##note from proteolytic cleavage of semenogelin during
liquefaction of semen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from proteolytic cleavage of semenogelin during
liquefaction of semen
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#region semenogelin short repeat 2\
#region semenogelin long repeat 1\
#region semenogelin long repeat 2\
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##residues 108-138 ##label SEI
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#cross-references MUID:93185635
#accession S29380
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p_position 20q12-20q13.1
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#journal Gene (1986) 50:173-184
#title Region E3 of human adenoviruses; differences between the oncogenic adenovirus-3 and the non-oncogenic adenovirus-2.
#cross-references_MUID:87219876
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                                       absent\
#disulfide_bonds interchain #status experimental
#length 462 #molecular-weight 52117 #checksum 9901
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subnitted to the EMBL Data Library, April 1995
Sequence analysis of the E3 region and fiber gene of
adenovirus 7h.
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##residues 1-136 ##label KAJ
##cross_references EMBL:248954; NID:g762955; PID:g762964
##experimental_source strain 87-922
##experimental_source strain 87-922
CLASSIFICATION #superfamily adenovirus early E3B 14K protein
#length 136 #molecular-weight 15275 #checksum 7906
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##molecule_type_DNA
##molecule_type = 1-136 ##label SIG
##ross_references GB:M15952; NID:g209901; PID:g209910
##cross_references GB:M15952; NID:g209901 PID:g209910
##cross_references GB:M15952; NID:g209901 PID:g209910
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early E3B 14K protein - human adenovirus 3
early E3B 15.3K protein
#region semenogelin short repeat 3\
#binding_site carbohydrate (Asn) (companies)
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#length 136 #molecular-weight 15266
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Pred. No. 1.93e+01;
2; Mismatches 0
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Best Local Similarity 71.4%;
Matches 5; Conservative
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Best Local Similarity 71.4%;
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Matches 6; Conservative
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#product beta-glucosidase #status predicted #label MAT\
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Biochem. J. (1996) 315:523-531
Prediction from sequence comparisons of residues of factor H
involved in the interaction with complement component C3b.
865551
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#superfamily complement factor H; complement factor H repeat
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Nucleotide sequence of Candida pelliculosa beta-glucosidase
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beta-glucosidase (EC 3.2.1.21) precursor - yeast (Pichia
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28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change
01-Nov-1996
                                                                                       $65551 #type fragment factor H - bowine (fragment) #formal_name Bos primigenius taurus #common_name cattle 19.Mar-1997 #sequence_revision 25-Apr-1997 #text_change 16-Dec-1998
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Kohchi, C.; Toh-e, A.
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#accession B23783
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Similarity 57.1%;
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21,34,74,97,230,
271,328,335,537,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #authors Basler, C.F.; Droguett, G.; Horwitz, M.S.
#journal Gene (1996) 170:249-254
#title Sequence of the immunoregulatory early region 3 and flanking sequences of adenovirus type 35.
#cross-references MUID:96235144
#accession JC4773
                                                                                                                                                                                                                                 ERAD74 #type complete early E3B 15.3K protein - human adenovirus 7 (strain Gomen) #formal_name Mastadenovirus h7 #common_name human adenovirus
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                                                                                                                                                                                                                                                                                                                                                                                 Hong, J.S.; Mullis, K.G.; Engler, J.A.
Virology (1988) 167:545-553
Characterization of the early region 3 and fiber genes of
#binding_site carbohydrate (Asn) (covalent) #status
                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                 host Homo sapiens (man)
31.Mar-1990 #sequence_revision 31-Mar-1990 #text_change
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    08-Sep-1997
JC4773
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#length 135 #molecular-weight 15363 #checksum 8529
                                  #checksum 8818
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E3 gene encoding hypothetical 15.3k protein - human
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Pred. No. 3.28e+01;
1; Mismatches 1; Indels
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                                                               Score 41; DB 1; Length 825;
Pred. No. 1.93e+01;
2; Mismatches 0; Indels
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##cross-references GB:U32664; NID:9984529; PID:9984538
T This protein inhibits TNF-alpha cytolysis.
                                #molecular-weight 89560
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#accession E31830
               predicted
#length 825 #mo
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Matches 5; Conservative
                                                              83.7%;
Similarity 71.4%;
5; Conservative
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1 QNKISYQ 7
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hypothetical protein, 15.3K - human adenovirus 11 #formal_name Mastadenovirus h11 #common_name human adenovirus
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**Authors Mei, Y.F.; Wadell, G. #$
#journal Wirology (1993) 194:453-462
#fille Hemagglutination properties and nucleotide sequence analysis
#cross-references MUID:93276532
#contents Adllp, Slobitski
#accession C37476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence extracted from NCBI backbone (NCBIN:132883, NCBIP:132886)
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                                                                                                                                                                                   21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 03-May-1996 C37476
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#formal_name Escherichia coli
28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change
14-Nov-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #Superfamily adenovirus early E3B 14K protein
#length 135 #molecular-weight 15293 #checksum 7034
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#title Analysis of the Escherichia coli genome VI:
#cross-references MUID:95334362
#accession S56414
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1; Mismatches 1
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#type complete
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##molecule_type nucleic acid
##residues 1-135 ##label MEI
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#authors Lintermans, P.F.; Bertels, A.; Schlicker, C.; Deboeck, F.;

#authors Lintermans, P.F.; Bertels, A.; Schlicker, C.; Deboeck, F.;

Charlier, G.; Pohl, P.; Norgren, M.; Normark, S.; Van

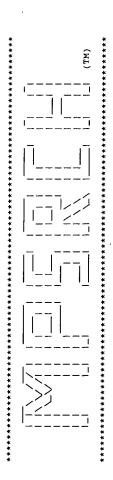
#ontagu, M.; De Greve, H.

#storeal, J. Bacteriol, 1991) 173:386-3373

#title Jacteriol, Characterization, and nucleotide sequence of the F17-G gene, which determines receptor binding of Escherichia coli F17 fimbriae.

#cross-references MulD:91258316

#accession A42359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##residues 1-326 ##label ARN
##cross-references GB:AE001327; GB:AE001273; NID:q3328999; PID:g3329000
##experimental_source serotype D, strain UW-3/Cx
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                                                    ##NOCALULE_CYPC Dim.
##TECSIGUES 1-142 ##label BLAT
##cross.references GB:AE000491; GB:U00096; NID:g2367357; PID:g1790633;
##Cross.references UMGP:b4189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #authors Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, W.P.; Olinger, L.; Tatusov, R.L.; Zhao, O.; Koonin, E.V.; Davis, R.W. science (1998) 282:754-759 #journal Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             442359 #type complete fimbrial adhesin F17-G precursor - Escherichia coli #formal_name Escherichia coli 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 24-Sep-1998
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(serotype D, strain UW3/Cx)
#formal_name Chlamydia trachomatis
13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change
21-Nov-1998
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#length 326 #molecular-weight 35553 #checksum 5831
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#length 142 #molecular-weight 16034 #checksum 6007
preliminary; nucleic acid sequence not shown; translation not shown
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Pred. No. 3.28e+01;
1; Mismatches 1; Indels
                                                                                                                             ##experimental_source strain K-12, substrain MG1655
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Matches 5; Conservative
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

MasPar time 2.09 Seconds 94.559 Million cell updates/sec Thu Oct 28 11:30:07 1999; Run on:

Tabular output not generated.

>US-09-081-707-11 (1-7) from US09081707.pep 49 Description: Perfect Score:

1 QNKISYQ 7 Sequence: 77977 seqs, 28268293 residues Searched:

PAM 150 Gap 15

Scoring table:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

swiss-prot37 1:swissprot

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 20.894; Variance 18.348; scale 1.139

# SUMMARIES

Pred. No.	5.26e-01	5.26e-01	3.50e+00	3.50e+00	6.44e+00	6.44e+00	1.17e+01	1.17e+01	1.17e+01	1.17e+01	1.17e+01	1.17e+01	2.10e+01	2.10e+01	2.10e+01	2.10e+01	2.10e+01	2.10e+01	3.71e+01	3.71e+01	3.71e+01	3.71e+01	3.71e+01
Description	SEMENOGELIN II PRECURS	Π	HYPOTHETICAL PROTEIN M	SEMENOGELIN I PROTEIN	EARLY E3 15.3 KD PROTE	BETA-GLUCOSIDASE PRECU	HYPOTHETICAL 12.1 KD P	EARLY E3 15.3 KD PROTE	HYPOTHETICAL 16.0 KD P	EARLY 65 KD PROTEIN.	DNA TOPOISOMERASE I (E	MAJOR NONSTRUCTURAL PR	FLAGELLAR BASAL-BODY R	XYLOSE REPRESSOR.	ACETYLCHOLINE RECEPTOR	GLUCOSE-6-PHOSPHATE IS	PUTATIVE SERINE/THREON	NONSENSE-MEDIATED MRNA	HYPOTHETICAL 25.6 KD P	HYPOTHETICAL TRANSCRIP	HYPOTHETICAL PROTEIN M	HYPOTHETICAL PROTEIN M	CMP-N-ACETYLNEURAMINAT
ΩI	SEM2_HUMAN	SEM2_MACMU	Y127_MYCGE	SEM1_HUMAN	E314_ADE03	BGLS_HANAN	DGLA_STAXY	E314_ADE07	YJFO_ECOLI	VH65_NPVAC	TOP1_MYCGE	VM3_REOVD	FLGB_BACSU	XYLR_BACSU	ACH6_CAEEL	G6PI_ACICA	PKNB_MYCLE	NMD2_YEAST	YMW7_YEAST	YHCK_ECOLI	Y326_MYCGE	Y028_METJA	CAG4_MOUSE
DB	-	Н	-	Н	П	Н	Н	Н	Н	Н	ч	Н	Н	Н	۲	-	Н	Н	П	Н	Н	Н	Н
Length	582	106	145	462	136	825	101	135	142	553	709	719	129	384	487	557	622	1089	221	263	295	319	337
Query Match	91.8	91.8	85.7	85.7	83.7	83.7	81.6	81.6	81.6	81.6	81.6		79.6	9.64	9.62	9.62	79.6	79.6		77.6	•	77.6	77.6
Score	45	45	42	42	41	41	40	40	40	40	40	40	38	36	39	39	39	39	38	38	38	38	38
Result No.		7	m	4	Ŋ	9	7	<b>6</b> 0	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

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3.71e+01	3.71e+01	3.71e+01	3.71e+01	3.71e+01	3.71e+01	3.71e+01	3.71e+01	3.71e+01	3.71e+01	3.71e+01	6.47e+01									
CITRATE SYNTHASE (EC 4	SYNAPTONEMAL COMPLEX P	ENOLASE (EC 4.2.1.11)	PROTEIN KINASE CLK3 (E	PROTEIN KINASE CLK3 (E	PUTATIVE SERINE CARBOX	GLUCOSE INHIBITED DIVI	ATP-DEPENDENT DNA HELI	HYPOTHETICAL PROTEIN M	GLUCAN ENDO-1, 3-BETA-G	CHECKPOINT SERINE/THRE	HYPOTHETICAL 25.7 KD P	PHOSPHATE-BINDING PERI	RIBONUCLEOSIDE-DIPHOSP	PHOSPHATE-BINDING PERI	HYPOTHETICAL 44.3 KD P	WALL-ASSOCIATED PROTEI	HYPOTHETICAL 59.4 KD P	ATP-DEPENDENT DNA HELI	PREPROTEIN TRANSLOCASE	DNA POLYMERASE (EC 2.7
CISY_HELPY	SC65_RAT	ENO1_SCHPO	CLK3_RAT	CLK3_MOUSE	YYP3_CAEEL.	GIDA_MYCPN	REP_BUCAP	Y32E_MYCPN	E13B_TRIHA	BUB1_YEAST	YVQH_BACSU	PSTS_HAEIN	RIR2_HELPY	PSTS_ECOLI	YLJ0_CAEEL	WAPA_STRMU	YFK9_YEAST	REP_ECOLI	SECA_PAVLU	DPO1_KLULA
П.	٠,	7	Н	1	П	٦	٦	7	7	7	٦	н	7	ч	7	П	Н	н	Н	Н
426	431	439	490	490	574	612	658	999	762	1021	225	334	341	346	382	445	510	673	891	992
77.6	77.6	77.6	77.6	77.6	77.6	77.6	77.6	77.6	77.6	77.6	75.5	75.5	75.5	75.5	75.5	75.5	75.5	75.5	75.5	75.5
38	38	38	38	38	38	38	38	38	38	38	37	37	37	37	37	37	37	37	37	37
24	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

#### ALIGNMENTS

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SEMG1 OR SEMG.
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Y127_MYCGE
P47373;
                                        01-0CT-1996
                                                   01-0CT-1996
01-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 QNKISY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEM1_HUMAN
P04279;
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions along as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EUR. J. BIOCHEM. 245:25-31(1997).
-!- FUNCTION: PARTICIPATE IN THE FORMATION OF A GEL MATRIX ENTRAPPING
THE ACCESSORY GLAND SECRETIONS AND EJACULATED SPERMATOZOA.
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE: 97274635.
ULVSBACK M., LUNDWALL A.;
"Cloning of the semenogelin II gene of the rhesus monkey.
Duplications of 360 bp extend the coding region in man, rhesus monkey and baboon.";
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      MACACA MULATTA (RHESUS MACAQUE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; CERCOPITHECIDAE; CERCOPITHECINAE; MACACA.
                                                                                                                                                              60 AA TANDEM REPEATS, TYPE I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                 Score 45; DB 1; Length 582;
Pred. No. 5.26e-01;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 45; DB 1; Length 706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                            EMBL; M81651; G307418; -.
EMBL; M81652; G338239; -.
EMBL; Z47556; E82662; -.
PIN; A43412.
MIM; 182141; -.
SEMEN; SEMINAL VESICLE; REPEAT; SIGNAL; GLYCOPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEMEN; SEMINAL VESICLE; REPEAT; SIGNAL; GLYCOPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 5.26e-01;
1; Mismatches 0;
                                                                                                         SEMENOGELIN II.
REPEAT-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEMENOGELIN II.
9D5897A8 CRC32;
                                                                                                                                                                                   PROBABLE.
DD20304E CRC32;
                                                                                                                                                                                                                                                                                                                             706 AA
                                                                                                                                                                                                                                                                                                                                                             UPDATE)
                                                                                                         SEMENOGELIN
          or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UP
15-JUL-1998 (REL. 36, LAST ANNOTATION
                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                  2-2.
3-2.
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: 79875 MW;
                                                                                                                                                                                                                                                                                                                                                                                  SEMENOGELIN II PRECURSOR (SGII)
                                                                                                                                                                                              65445 MW;
                                                                                                                                                                                                                 91.8%;
ilarity 85.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91.8%;
Similarity 85.7%;
6; Conservative
                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X92589; E208370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24
706 AA;
                                                                                                                                                   201
261
501
272
582 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 6; Conser
                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                             343 ENKISYQ 349
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1 QNKISYQ 7
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15-JUL-1998
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Q95196;
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                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                              SEQUENCE
                                                                                                                   DOMAIN
REPEAT
REPEAT
                                                                                              SIGNAL
                                                                                                                                                              DOMAIN
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                                                                                                                                                                                                                                                       STRAIN=ATCC 33530 / G-37;

STRAIN=ATCC 33530 / G-37;

STRAIN=ATCC 33530 / G-37;

STRAIN=ATCC 33530 / G-37;

MEDLINE, 96026346.

FRASER C.M., GOCAYUB J.D., WHITE O., ADAMS M.D., CLAYTON R.A.,

FLEISCHMANN R.D., BULT C.J., KERLAVAGE A.R., SUTTON G., KELLEY J.M.,

FRITCHMAN J.L., WEIDMAN J.F., SAMLIK K.V., SANDISKY M., FUHRMINN J.L.,

TOMB J.-F., DOUGHERTY B.A., SAUDEK D.M., PHILLIPS C.A., MERRICK J.M.,

TOMB J.-F., NATTH H.O., HUTCHISON C.A. III, VENTER J.C.,

"The minimal gene complement of Mycoplasma genitalium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=BLOOD;
MEDLINE; 92388176.
ULVSBAECK M., LAZURE C., LILJA H., SPURR N.K., RAO V.V., LOEFFLER C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE; 89109115.
LILJA H., ABRAHAMSSON P.-A., LUNDWALL A.;
LILJA H., ABRAHAMSSON P.-A., LUNDWALL A.;
Semenogelin, the predominant protein in human semen. Primary
structure and identification of closely related proteins in the male
accessory sex glands and on the spermatozoa.";
J. BIOL. CHEM. 264:1894-1900(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOFATION UPDATE)
SEMENOGELIN I PROTEIN PRECURSOR (SGI) [CONTAINS: SEMINAL BASIC
PROFEIN, ALPHA-INHIBIN-92; ALPHA-INHIBIN-31].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                        BACILLUS/CLOSTRIDIUM GROUP; MOLLICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 42; DB 1; L
Pred. No. 3.50e+00;
0; Mismatches A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, V...
HYPOTHETICAL PROTEIN.
HYPOTHETICAL PROTEIN.
FONTENCE 145 AA: 16565 MW; D203137F CRC32;
                                                                      LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           462 AA
AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -:- SIMILARITY: TO B.SUBTILIS YOGZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04, CREATED)
                                               (REL. 34, CREATED)
                                                                                                                                                                                        BACTERIA; FIRMICUTES; BACILLI
MYCOPLASMATACEAE; MYCOPLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 85.7%;
Local Similarity 100.0%;
es 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U39691; G1045807; -.
                                                                                                                   HYPOTHETICAL PROTEIN MG127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
STANDARD;
                                                               (REL. 34, 1
(REL. 34, 1
                                                                                                                                                                   MYCOPLASMA GENITALIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-MAR-1987 (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39
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                                                                                                                                                                                                                                                                                                                                                                                      PROC. NATL. ACAD. SCI. U.S.A. 82:4041-4044(1985).
-!- FUNCTION: SEMENOGELIN I IS THE PREDOMINANT PROTEIN IN HUMAN SEMEN.
IT PARTICIPATES IN THE FORMATION OF A GEL MATRIX ENTRAPPING THE
ACCESSORY GLAND SECRETIONS AND EJACULATED SPERMATOZOA. FRAGMENTS
OF SEMENOGELIN AND/OR FRAGMENTS OF THE RELATED PROTEINS NAY
CONTRIBUTE TO THE ACTIVATION OF PROGRESSIVE SPERM MOVEMENTS AS
THE GEL-FORMING PROTEINS ARE FRAGMENTED BY THE KALLIKREIN-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: ALPHA-INHIBIN-92 AND ALPHA-INHIBIN-31, DERIVED FROM THE PROTEOLYTIC DEGRADATION OF SEMENOGELIN, INHIBIT THE SECRETION OF PITUITARY FOLLICLE-STIMULATING HORMONE.
                Gene structure of semenogelin I and II. The predominant proteins in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42 AA REPEAT 1.

42 AA REPEAT 2.

58 AA REPEAT 1.

58 AA REPEAT 2.

42 AA REPEAT 3.

5 > 7 (LESS COMON GENETIC VARIANT).

K -> N (IN REF. 2).

W; C87515C7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEMENOGELIN I.
PYRROLIDONE CARBOXYLIC ACID (PROBABLE).
ALPHA-INHIBIN-92.
                                 Nan semen are encoded by two homologous genes on chromosome 20."; BIOL. CHEM. 267:18080-18084(1992).
                                                                                                                                                                                                              DELIDAH N.G., RAMASHARMA K., SAIRAM M.R., CHRETIEN M.; "Partial amino acid sequence of a human seminal plasma peptide with inhibin-like activity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: OCCURS IN DISULFIDE-LINKED COMPLEXES WHICH MAY ALSO CONTAIN TWO LESS ABUNDANT 71- AND 76-KD SEMENOGELIN-RELATED
                                                                                                                                                                                                                                                                                                                       MEDLINE: 85216629.
LI C.H., HAMMONDS R.G., RAMASHARMA K., CHUNG D.;
"Human seminal alpha inhibins: isolation, characterization, and
                                                                                                           LILJA H., JEPPSSON J.-O.; Amino acid sequence of the predominant basic protein in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT; SIGNAL; POLYMORPHISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALPHA-INHIBIN-31.
SEMINAL BASIC PROTEIN.
INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- TISSUE SPECIFICITY: SEMINAL VESICLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52131 MW;
                                                                                                                                                            FEBS LETT. 182:181-184(1985).
                                                                                                                                                                                                                                                                             FEBS LETT. 167:98-102(1984).
                                                                                                                                                                                                                          SEIDAH N.G., RAMASHARMA K.,
                                 human semen are encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; J04440; G338019; -.
EMBL; Z47556; E133812; -.
EMBL; M81650; G487420; -.
HANSMANN I., LUNDWALL A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VESICLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A03254; WTHUB.
PIR; A31489; A31489.
MIM; 182140; -.
                                                                               SEQUENCE OF 108-159.
                                                                                                                                                                                             SEQUENCE OF 108-138.
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423
462 AA;
                                                                                                                                                                                                                                                                                                           68-159.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLYPEPTIDES.
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                                                                                                                                                plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEASE.
                                                                                                                                                                                                                                                                                          [5]
SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                            structure
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DISULFID
REPEAT
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MOD_RES
PEPTIDE
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Length 462;

Score 42; DB 1; L Pred. No. 3.50e+00;

Query Match 85.7%; Best Local Similarity 100.0%;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAS C., AKUSJARVI G., PETTERSSON U.; "Addenovinus 3 fiber polypeptide gene: implications for the structure of the fiber protein."; by the fiber protein."; J. VIROL. 53:672-678(1985).
 Gaps
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE; 87219876.
SIGNAS C., AKUSJARVI G., PETTERSSON U.;
Region E3 of human adenoviruses; differences between the oncogenic adenovirus-3 and the non-oncogenic adenovirus-2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 90156523.
HORTON T.H., TOLLEFSON A.E., WOLD W.S.M., GOODING L.R.;
"A protein serologically and functionally related to the group C E3
14,700-kilodalton protein is found in multiple adenovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1988 (REL. 06, CREATED)
01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
BETA-GLUCOSIDASE PRECURSOR (EC 3.2.1.21) (GENTIOBIASE) (CELLOBIASE)
                                                                                                                                                                                                                        VIRUSES; DSDNA VIRUSES, NO RNA STAGE; ADENOVIRIDAE; MASTADENOVIRUS.
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   Indels
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o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136 AA; 15266 MW; 759E40EA CRC32;
                                                                                                 E314_ADE03 STANDARD; PRT; 136 AA. P11315; 01-JUL-1989 (REL. 11, CREATED) 01-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE) 01-AUG-1990 (REL. 15, LAST ANNOTATION UPDATE) EARLY E3 15.3 KD PROTEIN.
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BETA-D-GLUCOSIDE GLUCOHYDROLASE).
0;
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 128-136 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDENTIFICATION OF PROTEIN.
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M15952; G209910; -.
                                                                                                                                                                                                       HUMAN ADENOVIRUS TYPE 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X01998; G583843; -
EMBL; M12411; G209927; -
PIR; A27623; ERAD29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                            GENE 50:173-184(1986).
                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 85108162
                             284 NKISYQ 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 QSKISYE 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |:||||:
QNKISYQ 7
                                                       NKISYO 7
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BGLS_HANAN
P06835;
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                                                              "Glucose kinase-dependent catabolite repression in Staphylococcus
         STRAIN-DSM 20267 / C2A;
MEDLINE; 96042090.
WAGNER E., MARCANDIER S., EGETER O., DEUTSCHER J., GOETZ F.,
BRUCKNER R.;
                                                                                                  -!- SIMILARITY: BELONGS TO THE UPF0045 FAMILY
                                                                        losus.";
BACTERIOL. 177:6144-6152(1995)
                                                                                                                                                                                                                          EMBL; X84332; E147899; -. HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                            35 QGKIDYQ 41
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                                                                      MEDLINE; 86016087.

KOHGHI C., TOH-E A.;

Nuclectide sequence of Candida pelliculosa beta-glucosidase gene.";

NUCLEIC ACIDS RES. 13:6273-6282(1985).

-! CATALYTIC ACIIVITY: HYDROLYSIS OF TERMINAL, NON-REDUCING BETA-D-GLUCOSE RESIDUES WITH RELEASE OF BETA-D-GLUCOSE.

-! PATHWAY: CELLULOSE DESRADATION.
-! SUBUNIT: HOMOLETRAMER.
                                                                                                                                                                                                                                                                                                               PIR; B23783; GLHQ.
PROSITE; PS60775; GLYCOSYL_HYDROL_F3; 1.
PFAM; PF00933; 91ycosyl_hydr14; 1.
HYDROLASE; GLYCOSIDASE; CELLULOSE DEGRADATION; GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
HANSENULA ANOMALA (YEAST) (CANDIDA PELLICULOSA).
EUKARYOTA: FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
SACCHAROMYCETACEAE; PICHIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                          -! - SIMILARITY: BELONGS TO FAMILY 3 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 825;
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Pred. No. 6.44e+00;
2; Mismatches 0
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BETA-GLUCOSIDASE.
BY SIMILARITY.
POTENTIAL.
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211
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718
                                                SEQUENCE FROM N.A. STRAIN=ACETAETHERIUS;
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825 AA;
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Best Local Similarity
Matches 5; Conser
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667
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Q56200;
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ACT_SITE
CARBOHYD
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Gaps

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Score 40; DB 1; Length 107; Pred. No. 1.17e+01; 0; Mismatches 2; Indels

81.6%; ilarity 71.4%; Conservative

107 AA; 12053 MW; C3963FD1 CRC32;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                          serotypes.";
J. VIROL. 64:1250-1255(1990).
-!- FUNCTION: PROTECT VIRUS-INFECTED CELLS FROM TWF-INDUCED CYTOLYSIS.
                                                                                                                                                                                                                                                                                                                                                          E3
                                                                                                                                           VIRUSES; DSDNA VIRUSES, NO RNA STAGE; ADENOVIRIDAE; MASTADENOVIRUS.
                                                                                                                                                                                             STRAIN=GOMEN;
MEDLINE; 89073758.
HONG J.S., MULLIS K.G., ENGLER J.A.;
"Characterization of the early region 3 and fiber genes of Ad7.";
VIROLOGY 167:545-553(1988).
                                                                                                                                                                                                                                                                                                                   MEDLINE; 90156523.
HORTON T.H., TOLLEFSON A.E., WOLD W.S.M., GOODING L.R.;
"A protein serologically and functionally related to the group C
14,700-kilodalton protein is found in multiple adenovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: TO EQUIVALENT PROTEIN IN OTHER ADENOVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40; DB 1; Length 135; Pred. No. 1.17e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135 AA; 15363 MW; F1191DBF CRC32;
                                                                    14, LAST SEQUENCE UPDATE)
15, LAST ANNOTATION UPDATE)
                  135 AA
                    PRT;
                                                   01-APR-1990 (REL. 14, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81.6%;
71.4%;
                                                                                                                                                                                                                                                                                                      IDENTIFICATION OF PROTEIN.
                                                                                     01-AUG-1990 (REL. 15, LAS'
EARLY E3 15.3 KD PROTEIN.
HUMAN ADENOVIRUS TYPE 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M23696; G576460; --
PIR; E31830; ERAD74.
EARLY PROTEIN.
SEQUENCE 135 AA; 15363
                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                              SEQUENCE FROM N.A.
LT 8
E314_ADE07
P15135;
                                                                    01-APR-1990
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STAPHYLOCOCCUS XYLOSUS.
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE; STAPHYLOCOCCUS.

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15-JUL-1998 (REL. 36, CREATED) 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE) 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE) 17-JUL-1998 (REL. 36, PROTEIN IN GIKA 3'REGION (ORF2).

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TOP1_MYCGE
P47368;
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    Gaps
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                                                                                                                                                                                                                                                                                                              BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
ESCHERICHIA.
  0;
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0
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01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
HYPOTHETICAL 16.0 KD PROTEIN IN AIDB-SGAT INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).
VIRUSES; DSDNA VIRUSES, NO RNA STAGE; BACULOVIRIDAE;
NUCLEOPOLYHEDROVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Sequence and temporal appearance of the early transcribed baculovirus gene HE65.";
J. VIROL. 67:5867-5872(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40; DB 1; Length 142;
Pred. No. 1.17e+01;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
STRAIN-KI2 / MG1655;
MEDLINE; 95343462.
BURLAND V.D., PLUNKETT G. III, SOFIA H.J., DANIELS D.L.,
    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78C83A3C CRC32;
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01-FPB-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
EARLY 65 KD PROTEIN.
  1; Mismatches
                                                                                                                                                            142 AA
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                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142 AA; 16034 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE000491; G1790633; -. ECOGENE; EG12489; YJFO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.6%;
Similarity 57.1%;
4; Conservative
  Conservative
                                                                                                                                                          STANDARD;
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                                                                                                                                                  YJFO_ECOLI STANI
P39297;
01-FEB-1995 (REL. 3
01-FEB-1995 (REL. 3
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Best Local Similarity
Matches 4; Conser
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SEQUENCE FROM N.A.
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                                      67
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1 QNKISYQ 7
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Q08539;
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                                      61
Matches
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SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

SETALINEATCS 3330 / G-37;

MEDLINE, 96026346.

MEDLINE, 96026346.

FRASER C.M., GOCATNE J.D., WHITE O., ADAMS M.D., CLAYTON R.A.,

FLEISCHMANN R.D., BULT C.J., KERLAVAGE A.R., SUTTON G., KELLEY J.M.,

FRITCHMAN J.L., WEIDMAN J.F., SANLDE K.W., SANDUSKY M., FUHRMANN J.L.,

NGUYEN D.T., UTTERBACK T.R., SAUDEK D.M., PHILLIPS C.A., MERRICK J.M.,

TOMB J.-F., DOUGHERTY B.A., BOTT K.F., HU P.-C., LUCIER T.S.,

The minimal gene complement of Mycoplasma genitalium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. BACTERIOL. 175:7918-7930(1993).

-!- FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES LEADS TO THE CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER.

-!- CATALYTIC ACTIVITY: ATP-INDEPENDENT BREAKAGE OF SINGLE-STRANDED DNA, FOLLOWED BY PASSAGE AND REJOINING.
-!- SUBBUNIT: MONOMER (BY SIMILARITY).
-!- WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA BACKBONE BOND, IT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
01A TOPOLSOMERASE I (EC 5.99.1.2) (OMEGA-PROTEIN) (RELAXING ENZYME)
(UNTWISTING_ENZYME) (SWIVELASE).
MEDLINE; 94303173.

AYRES M.D., HOWARD S.C., KUZIO J., LOPEZ-FERBER M., POSSEE R.D.;
The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.";
VIROLOGY 202:586-605(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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STRAIN-AATC 33530 / G-37;
MEDLINE; 94075230.
PETERSON S.N., HUP.P.-C., BOTT K.F., HUTCHISON C.A. III;
"A survey of the Mycoplasma genitalium genome by using random
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; MOLLICUTES;
MYCOPLASMATACEAE; MYCOPLASMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40; DB 1; Le
Pred. No. 1.17e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    553 AA; 65576 MW; 420D4413 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        709 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X73577; G313680; -. EMBL; L22858; G559174; -. PIR; S35872; S35872.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MYCOPLASMA GENITALIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    315 QNKITY 320
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1 QNKISYQ 7
                       FLGB_BACSU P24500;
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                                                                                                                                                                                                                                                                           SEQUENCE F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P16557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
  RESULT
                            g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 89204900.
WIENER J.R., BARTLETT J.A., JOKLIK W.K.;
"The sequences of reovirus serotype 3 genome segments M1 and M3 encoding the minor protein mu 2 and the major nonstructural protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mu NS, respectively";
VIROLOGY 169:293-304(1989).
-!- FUNCTION: THE MU-NONSTRUCTURAL PROTEIN IS A SS RNA-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
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                                                                                                                                                                                                                                                                                                                                                                                           DNA CLEAVAGE (BY SIMILARITY).; 18063FDC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 40; DB 1; Length 719;
Pred. No. 1.17e+01;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 81.6%; Score 40; DB 1; Length 709; 57.1%; Pred. No. 1.17e+01; rative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VIRUSES; DSRNA VIRUSES; REOVIRIDAE; ORTHOREOVIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  714DDF6E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-1989 (REL. 12, CREATED)
01-0CT-1989 (REL. 12, LAST SEQUENCE UPDATE)
01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         719 AA
                                                                                                                                                                                                                                                                                                PS00396; TOPOISOMERASE_I_PROK; 1.
                                                                                                                                                                                                                                                                                                                                                                   ISOMERASE; TOPOISOMERASE; DNA-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BLOCKED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NONSTRUCTURAL PROTEIN; RNA-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / STRAIN DEARING)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAJOR NONSTRUCTURAL PROTEIN MU-NS.
                                                                                                                                                                                                                                                                                                                   PFAM; PF01131; Topoisom_bac; 1. HSSP; P06612; 1ECL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 719 AA; 79960 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                82544 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 71.4%;
5; Conservative
                                                                                                                                                                                                     EMBL; U39691; G1045802; -. EMBL; U02134; G409912; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Conservative
                                                                                                                                                                                                                                                   EMBL; U02242; G407259; -. 
TIGR; MG122; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M27262; G333690; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B30179; MNXR3D
                                                                                                                                                                                                                                                                                                                                                                                                              709 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   577 ENKVNYQ 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REOVIRUS (TYPE 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  658 QNQITYQ 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : | |::||
1 ONKISYO 7
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| QNKISYQ 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LT 12
VM3_REOVD
                                                                                                                                                                                                                                                                                                                                                                                           ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                PROSITE;
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SPER BURRED DAY BURRED 
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                                                                                                                                                                                                                                                                               ZUBERI A.R., YING C., BISCHOFF D.S., ORDAL G.W.; "Gene-protein relationships in the flagellar hook-basal body complex of Bacillus subtilis: sequences of the flgB, flgC, flgG, fliE and flip aggre "."
                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=W23;
MEDLINE; 89297732.
KREUZER P., GABERTNER D., ALLMANSBERGER R., HILLEN W.;
KIROTZER P., GABERTNER D., ALLMANSBERGER R., HILLEN W.;
MIdentification and sequence analysis of the Bacillus subtilis W23
xylR gene and xyl operator.";
J. BACTERIOL. 171:3840-3845(1989).
                                                                                                                                                                      BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
BACILLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BACILLUS SUBTILIS.
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
BACILLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 AA; 14443 MW; 550868EA CRC32;
                                  01-MAR-1992 (REL. 21, CREATED)
01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
FLAGELLAR BASAL-BODY ROD PROTEIN FLGB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1990 (REL. 15, CREATED)
01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          384 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M54965; G142915; -.
EMBL; 299112; E1185209; -.
PIR; JG0019; JG0019.
SUBTILIST; BG10237; FLGB.
PROSITE; PS00588; FLAGELLA_BB_ROD; 1.
PRAY, PF00460; f1g_bb_rod; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                      FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                  BACILLUS SUBTILIS.
                                                                                                                                                                                                                                                             91285431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102 QNQINYQ 108
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Matches
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                                                                                                                                                                                                                                                                                                                                         ö
-!- FUNCTION: TRANSCRIPTIONAL REPRESSOR OF XYLOSE-UTILIZING ENZYMES.
-!- SIMILARITY: BELONGS TO THE ROK (NAGC/XXLR) FAMILY.
                                                                                                                                                                                                 PIG. PROSITE: PSOILS: TOK; 1.
PROSITE: PSOILS: TOK; 1.
PRAMS. PFO0480; ROK; 1.
TRANSCRIPTION REGULATION; DNA-BINDING; REPRESSOR; XYLOSE METABOLISM.
DNA_BIND 29 48 H-T-H MOTIF (BY SIMILARITY).
SEQUENCE 384 Aa; 42295 MW; FEALAE85 CRC32;
                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAENORHABDITIS ELEGANS.
EUKARYOTA: METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
ACETYLCHOLINE RECEPTOR LIKE PROTEIN,
ALPHA-TYPE SUBUNT ACR-3.
EXTRACELULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-BRISTOL N2;
BAYLIS H.A., MATSUDA K., SQUIRE M.D., FLEMING J.T., HARVEY R.J.,
DARLINSON M.G., BARNARD E.A., SATTELLE D.B.;
SUBMITTED (OCT-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
-!- FUNCTION: POSSIBLE ACETYLCHOLINE RECEPTOR.
                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Y08637; E274054; -.
PROSITE: PS00236; NEUROTR_ION_CHANNEL; 1.
PFAM, PF00065; neur_chan; 1.
TRECEPTOR: POSTISYMAPTIC MEMBRANE; IONIC CHANNEL; GLYCOPROTEIN; TRANSMEMBRANE; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
ACETYLCHOLINE RECEPTOR LIKE PROTEIN, BETA-TYPE SUBUNIT ACR-3
                                                                                                                                                                                                                                                                                                       Score 39; DB 1; Length 384; Pred. No. 2.10e+01;
                                                                                                                                                                                                                                                                                                                                      0; Indels
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                     79.6%;
Similarity 57.1%;
4; Conservative
                                                                                                                                                                         EMBL; M27248; G143841; -. PIR; A32885; A32885.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233
252
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Best Local Similarity
Matches 4; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                    275 EKKVSYQ 281
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259
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1 QNKISYQ 7
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Q93149;
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FT DISULFID 151 165 BY SIMILARITY.

SQ SEQUENCE 487 AA; 56245 MW; 102629B3 CRC32;

Query Match 79.6%; Score 39; DB 1; Length 487;

Best Local Similarity 71.4%; Pred. No. 2.10e+01;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps
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214 RSKISYQ 220 ::|||||

::||||| 1 QNKISYQ 7 Search completed: Thu Oct 28 11:30:15 1999 Job time: 8 secs.

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                                                                                                                                                                                                                                                                           Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                         MPsrch_pp
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protein - protein database search, using Smith-Waterman algorithm

Thu Oct 28 11:30:33 1999; MasPar time 4.13 Seconds 92.427 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-081-707-11 (1-7) from US09081707.pep 49 Title: Description: Perfect Score:

Seguence:

1 ONKISYQ 7 PAM 150 Gap 15 Scoring table:

179066 seqs, 54579741 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

sptremb19 Database:

1:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human 5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle 9:sp\_phage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified 13:sp\_vertebrate 14:sp\_virus

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Mean 20.112; Variance 21.027; scale 0.956

## SUMMARIES

Pred. No.	2.94e-01	3.01e+00	3.01e+00	9.17e+00	9.17e+00	9.17e+00	1.58e+01	2.70e+01	2.70e+01	2.70e+01	2.70e+01	2.70e+01	2.70e+01	2.70e+01	2.70e+01	2.70e+01	2.70e+01	2.70e+01	4.56e+01	4.56e+01
Description	28 KDA MAJOR SURFACE A	PLASMID PIL2614 REPLIC	PORCINE INHIBITOR OF C	6 KDA ANTIGEN (FRAGMEN	GS60 ANTIGEN.	PEPTIDYLARGININE DEIMI	C18H7.8 PROTEIN.	ORF 15.3 KDA.	HYPOTHETICAL 20.1 KD P	MX1 PROTEIN.	MX2 PROTEIN.	MX3 PROTEIN.	MX1 PROTEIN.	RBTMX3.	RBTMX2.	CCP MODULES 3-12, WITH	VIRION SPIKE GLYCOPROT	VIRION SPIKE GLYCOPROT	T23G4.2 PROTEIN.	15.3 KDA PROTEIN.
<b>a</b>	085359	054429	029545	053465	051850	002849	061810	083121	065386	091192	098991	098992	066860	091197	091196	028085	066799	089853	018126	067732
DB	~	7	9	7	7	9	Ŋ	14	14	13	13	13	13	13	13	9	14	14	ß	14
Length DB	287	292	704	51	546	664	433	136	175	621	623	623	623	623	635	699	677	677	128	135
% Query Match	100.0	91.8	91.8	87.8	87.8	87.8	85.7	83.7	83.7	83.7	83.7	83.7	83.7	83.7	83.7	83.7	83.7	83.7	81.6	81.6
Score	49	45	45	43	43	43	42	41	41	41	41	41	41	41	41	41	41	41	40	40
Result No.	~	7	м	4	S	φ	7	∞	σ	10	11	12	13	14	15	16	17	18	19	20

RESULT 2

ID 054429
AC 054429
AC 054429
C 054429
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DE PLASMID PIL2614 REPLICATION PROTEIN
DE (HSDR), TYPE IC MODIFICATION SUBUNIT
DE (HSDR), TYPE IC MODIFICATION SUBUNIT
DE (HSDS), AND PHAGE BORTIVE INFECTION PROTEIN
DE (HSDS), AND PHAGE SHORTIVE INFECTION PROTEIN
DE (AB1420) GENES, COMPLETE CDS (HSDR) (HSDS)
OS LACTOCOCCUS LACTIS (STREPTOCOCCUS LACTIS).

YOP TRANSLOCATION J. 4.56e+01 ADHESIN PRECURSOR. 4.56e+01 ASPARGINE RICH PROTEI TYPE III RESTRICTION E 4.56e+01 GROUP 3 LEA PROTEIN MG 7.63e+01 CYTOCHROME B (FRAGMENT 7.63e+01 CYTOCHROME B (FRAGMENT 7.63e+01 COSMID F40E3 BURNING 7.63e+01 HYPOTHETICAL 47.3 KD P 7.63e+01 HYPOTHETICAL 47.3 KD P 7.63e+01 HYPOTHETICAL 70.1 KD P 7.63e+01 HYPOTHETICAL 120.1 KD 7.63e+01 HYPOTHETICAL 141.0 KD 7.63e+01 HYPOTHE	T; 287 AA.  TED) SEQUENCE UPDATE) ANNOTATION UPDATE) ANNOTATION, RICKETTSIALES; LICHIA.  A.F., MAHAN S.M., BURRIDGE M.J., 28 kDa surface antigen gene family 47:636-643(1998). 216502E CRC32; e 49; DB 2; Length 287; No. 2:94e-01; Mismatches 0; Indels 0; Gaps 0;
084563 099003 040148 026050 0442376 042376 042376 062072 010551 062070 062070 017460 0	GNM STTT SST FEAT S ST 12 24 ST 12 24 ST 12 24 ST 12 24 ST 12 34 ST 12 34 ST 12 ST 1
11.6 326 2 11.6 324 2 11.6 514 2 11.6 514 2 11.6 514 2 11.6 514 2 11.6 514 2 11.6 522 8 11.6 222 8 11.6 2	AARX; EEL. 08 EEL. 08 EEL. 08 EEL. 08 EEL. 108 EEL. 108 EEL. 08 EEL. 00 EEL. 0
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	RESULT OC ALC DE CONTROLL OC DE CONTROL OC DECENTROL OCOTRO OCOTROL OCOTRO OC

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SEQUENCE
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-!- FUNCTION: TRANSFERRINS AFE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USCHALY BICARBONATE.

-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.

BENEL: U36916; G10161330; --.

PROSITE; PS00206; TRANSFERRIN_1; 2.

PROSITE; PS00206; TRANSFERRIN_2; 1.

PROSITE; PS00207; TRANSFERRIN_3; 2.

PROSITE; PS00405; Lansferrin; 2.

SIGNAL; IRON TRANSPORT; GLYCOPROTEN), METAL-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PORCINE INHIBITOR OF CARBONIC ANHYDRASE. 2E961A99 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                            STRAIN=IL1403;
MEDLINE: 98101482.
SCHOULER C., CLIER F., LERAYER A.L., EHRLICH S.D., CHOPIN M.C.;
A type IC .. CLIER F., Londification system in Lactococcus lactis.";
J. BACTERIOL. 180:407-411(1998).
EMBL; U90222; G2865241; -.
                                                                                                                                                                                                                                                                                                                                               Gaps
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MEDELINE, 97254619.
WUEBBENS M.W., ROUSH E.D., DECASTRO C.M., FIERKE C.A.;
WUEBBENS M.W., ROUGH E.D., DECASTRO C.M., FIERKE C.A.;
"Cloning, sequencing, and recombinant expression of the porcine inhibitor of carbonic anhydrase: a novel member of the transferrin
             BACTERIA: FIRMICUTES: BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
LACTOCOCCUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
0
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ROUSH E.D., FIERKE C.A.;
"Purification and characterization of a carbonic anhydrase II inhibitor from porcine plasma.";
BIOCHEMISTRY 31:12536-12542(1992).
                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUS SCROFA (PIG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
ARTIODACTYLA; SUIFORMES; SUINA; SUIDAE; SUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 45; DB 6; Length 704;
Pred. No. 3.01e+00;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                       Length 292;
                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
PORCINE INHIBITOR OF CARBONIC ANHYDRASE PRECURSOR.
                                                                                                                                                                                                                                                                                                  Score 45; DB 2; L
Pred. No. 3.01e+00;
1; Mismatches 0
                                                                                                                                                                                                                                                           34223 MW; 9EEE797D CRC32;
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Similarity 71.4%;
5; Conservative
                                                                                                                                                                                                                                                                                                         91.8%;
85.7%;
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                                                                                                                                                                                                                                                                                                                                                    6; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                292 AA;
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1 QNKISYQ 7
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SEQUENCE FROM N.A.
                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                             23 QNKISYE 29
      PLASMID PIL2614
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
ARIIODACTYLA; RUMINANTIA; PECORA; BOVOIDEA; BOVIDAE; CAPRINAE; OVIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                   MEDLINE; 95027654.
MEDLINE; 95027654.
WELDON S.K., MOSIER D.A., SIMONS K.R., CRAVEN R.C., CONFER A.W.; Identification of a potentially important antigen of Pasteurella haemolytica.", VET. MICROBIOL. 40:283-291(1994).
BMBL; S74144; E155751; -..
NOW_TER 51 51
NOW_TER 51 51
SEQUENCE 51 AA; 5954 MW; 93E7B40E CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PASTEURELLA HAEMOLYTICA.
BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PASTEURELLACEAE;
                                                                                      6 KDA ANTIGEN (FRAGMENT).
PASTEDRELLA HAEMOLYTICA.
BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PASTEURELLACEAE;
PASTEURELLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.8%; Score 43; DB 2; Length 546; 71.4%; Pred. No. 9.17e+00; Arive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                 Length 51;
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SEQUENCE FROM N.A.
STRAIN=SEROTYPE 1;
STRAIN=ON X.C.
SUBMITTED (DEC-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U42028; G1353671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.002849 PRELIMINARY; PRT; 664 AA. 002849 O02849 O1-JUL-1997 (TREMBLREL. 04, CREATED) O1-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE) O1-AD-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE) PEPTIDYLARGININE DEIMINASE (EC 3.5.3.15)
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                               LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                               Score 43; DB 2; Lens
Pred. No. 9.17e+00;
2; Mismatches 0;
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51 AA.
                                    CREATED)
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PROTEIN-ARGININE DEIMINASE)
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01,
07,
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Conservative
                                    01,
01,
08,
                                                                                                                                                                                                                                                                                                                                                                   87.8%;
Similarity 71.4%;
5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
   PRELIMINARY;
                                  01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
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SEQUENCE FROM N.A.
TISSUE-WOOL FOLLICLES;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                         12 EDKISYQ 18
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ORF 15.3 KDA.
MASTADENOVIRUS
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Q65386
Q65386;
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SEQUENCE FROM N.A.

SEQUENCE TO N.2;

MEDLINE; 94150718

MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

MILSON R., AINSCOUGH R., ANDERSON K., BAYNELLO A., EULTON L.,

A CRATTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

A CRATTON M., DEAR S., DU Z., HILLIER M., JOHNSTON L.,

A DONES M., KERSHAW J., KIRSTEN J., LATETELLE P., O'CALLAGHAN M.,

A DARSONS J., PERCY C., RIFKEN L., ROOPRA B., SAUNDERS D., SHOWNKEEN R.,

A PARSONS J., PERCY C., RIFKEN L., SONNHAMBER D., SHOWNKEEN R.,

A THIERRY MIEG J., THOMAS K., VANDIN M., VANGHAN K., WATERSTON R.,

A WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

A WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

A WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

A WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

A WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

A WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

A WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

A WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

A WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

A WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

A WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

A WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

A WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

A WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

A WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

A WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

A WATSON A., WEINSTOR M., WILKINSON-SPROAT J., WOHLDMAN P.;

A WATSON A., WEINSTOR W., WATSON W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA; RHABDITINA; RHABDITIODEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
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0
ROGERS G.E., WINTER B.P., POWELL B.C., NESCI A.N.;
J. INVEST. DERMATOL. 0:0-0(0).
-!- CATALYTIC ACTIVITY: PROTEIN L-ARGININE + H(2)0 = PROTEIN
L-CITRULLINE + H(4).
EMBL; U85264; G2055390; -.
                                                                                                                                                                                                          Length 664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85.7%; Score 42; DB 5; Length 433; 71.4%; Pred. No. 1.58e+01; ative 2; Mismatches 0; Indels
                                                                                                                                                                                                        Score 43; DB 6; Length 664; Pred. No. 9.17e+00; 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
WATERSTON R.
SUBMITTED (MAY-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF067607; G3165526; -.
SEQUENCE 433 AA; 50343 MW; 47266C20 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IIN-WOLLAM A., FRONICK W.;
SUBMITTED (MAY-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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LAST ANNOTATION UPDATE)
                                                                                                                                                     664 AA; 74747 MW; 6813DB1B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        433 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1998 (TREMBLREL. 07,
01-AUG-1998 (TREMBLREL. 07,
01-NOV-1998 (TREMBLREL. 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01,
01,
08,
                                                                                                                                                                                                        7.8%;
Local Similarity 71.4%;
Nes 5; Conservative
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nes 5; Conservative
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(TREMBLREL. C
(TREMBLREL. C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                             232 QNKVSYE 238
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C18H7.8.
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061810
061810;
01-AUG-1998 (
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Q83121
Q83121;
01-NOV-1996 (
01-NOV-1996 (
01-NOV-1998 (
                                                                                                                             HYDROLASE.
SEQUENCE
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Best Local S
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Matches
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ID 08
AC 08
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DT 01
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EUKARYOTA; METAZOA; CHORDATA; VĘRTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI; EUTELEOSTEI; PROTACANTHOPTERYGII; SALMONIFORMES; SALMONIDAE;
                                                                                                                                                                                                                                                                                                                                      Gaps
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MEDLINE: 95302043.
BURNS T.M., HARDING R.M., DALE J.L.;
The genome organization of banana bunchy top virus: analysis of sSDNA components.";
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                                                              STRAIN-87-922;
MEDLINE; 96146733.
KAJON A. KAJON B. S. KAJON B. Sequence analysis of the E3 region and fiber gene of human adenovirus genome type 7h.";
VIROLOGY 215:190-196(1996).
EMBL; 248954; G762964;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41; DB 14; Length 175; Pred. No. 2.70e+01; 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                               Score 41; DB 14; Length 136;
Pred. No. 2.70e+01;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
101-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
HYPOTHETT.CAL. 20.1 KD PROTEIN.
BANANA BUNCHY TOP VIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
MXI PROTEIN.
VIRUSES; DSDNA VIRUSES, NO RNA STAGE; ADENOVIRIDAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TROBRIDGE G.D., LEONG J.A.;
"Characterization of a rainbow trout Mx gene.";
J. INTERFERON CYTOKINE RES. 15:691-702(1995).
EMBL. U30253; G905389; -.
PROSITE; PS00410; DYNAMIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. GEN. VIROL. 76:1471-1482(1995).
EMBL, L41574; G867679; -.
SPOTHETICAL PROTEIN
SEQUENCE 175 AA; 20111 MW; 48C78A21 CRC32;
                                                                                                                                                                                                                                  136 AA; 15275 MW; 87E42674 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               175 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VIRUSES; SSDNA VIRUSES; CIRCOVIRIDAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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PFAM; PF01031; dynamin_2; 1.
                                                                                                                                                                                                                                                                               83.7%;
ilarity 71.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83.7%;
Similarity 57.1%;
4; Conservative
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                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 4; Conserv
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                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     168 QNRITYH 174
                                                                                                                                                                                                                                                                                                                                                                                 62 QSKISYE 68
                                                                                                                                                                                                                                                                                                                                                                                                          |:||||:
1 QNKISYQ 7
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1 QNKISYQ 7
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Matches

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ONCORPATIONEM MYKISS (RAINBOW TROUT) (SALMO GAIRDNERI).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI; EUTELEOSTEI; PROTACANTHOPTERYGII; SALMONIFORMES; SALMONIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ONCORHYNCHUS MYKISS (RAINBOW TROUT) (SALMO GAIRDNERI).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI; EUTELEOSTEI; PROTACANTHOPTERYGII; SALMONIFORMES; SALMONIDAE;
                                                                                                      SALMO SALAR (ATLANTIC SALMON).
EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI; EUTELEOSTEI; PROTACANTHOPTERYGII; SALMONIFORMES; SALMONIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

TROBRIDGE G.D., CHIOU P.P., LEONG J.C.;

"Cloning of the rainbow trout (Oncorhynchus mykiss) Mx2 and Mx3 cDNAs and charactrization of trout Mx protein expression in salmon cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 623;
                                                                                                                                                                                                                                                                                                                                                                Length 623;
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Pred. No. 2.70e+01;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                              Score 41; DB 13; Length 62:
Pred. No. 2.70e+01;
1; Mismatches 1; Indels
                                                                                                                                                                                                SEQUENCE FROM N.A.
ROBERTSEN B., TROBRIDGE G.D., LEONG J.C.;
SUBMITTED B., TROBRIDGE G.D., LEONG J.C.;
SUBMITTED FOR G.D., GARL/GENBANK/DDBJ DATA BANKS.
BENBL, U66475; G1519384; -.
PROSITE; PSO0410; DYNAMIN; 1.
PRAM; PRO0350; dynamin; 1.
PERAM; PF00131; dynamin; 2: 1.
SEQUENCE 623 AA; 70895 MW; 99E0B5A5 CRC32;
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091196
091196;
091196;
01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1998 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
RETMX2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                  02, CREATED)
02, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
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EMBL; U47946; G1399454; -.

PROSITE; PS00410; DYNAMIN; 1.

PFAM; PF00350; dynamin; 1.

SEQUENCE 623 AA; 70962 MW; 8320E073 CRC32;
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 623 AA.
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 PRT;
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Similarity 71.4%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                  83.7%;
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Best Local Similarity 71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                    5; Conservative
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PRELIMINARY;
                                  01-FEB-1997 (TREMBLREL.
01-FEB-1997 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
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QNKISYQ 7
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                                                                                         PROTEIN.
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Best Local S
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ID 091197
AC 091197;
                                                                                                                                                                   SALMO.
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI; EUTELEOSTEI; PROTACANTHOPTERYGII; SALMONIFORMES; SALMONIDAE;
                                                                                                                                                                                                                                                                                                                                 BUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPIERYGII; NEOPIERYGII; TELEOSTEI; EUTELEOSTEI; PROTACANTHOPTERYGII; SALMONIFORMES; SALMONIDAE; SALMO.
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                                                                          Gaps
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ROBERTSEN B., TROBIDGE G.D., LEONG J.C.;

ROBERTSEN B., TROBIDGE G.D., LEONG J.C.;

RUCIOLING of the MX Genes of Atlantic Salmon (Salmo salar).";

L SUBMITTED (AUG-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.

DR FMALL, 106447; G1783385;

DR PROSITE; PSO0410; DYNAMIN; 1.

DR PROM; PFO0350; dynamin; 1.

DR PFAM; PFO1031; dynamin; 1.

DR PFAM; PFO1031; dynamin; 2; 1.

SEQUENCE 623 AA; 70923 MW; DAC2A40A CRC32;
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Pred. No. 2.70e+01;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83.7%; Score 41; DB 13; Length 623; 71.4%; Pred. No. 2.70e+01; ative 1; Mismatches 1; Indels
                                      Score 41; DB 13; Length 621;
Pred. No. 2.70e+01;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
ROBERTSEN B., TROBRIDGE G.D., LEONG J.C.;
SUBMITTED (ACC1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL, U66476; G1219386; -.
PROSITE; PSO0410; DYNAMIN; 1.
PRAM; PF00330; dynamin; 1.
PFAM; PF01031; dynamin; 2: 1.
SEQUENCE 623 AA: 70804 MW; B18012DA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                           01-FEB-1997 (TREMBLREL. 02, CREATED)
01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
     8F350554 CRC32;
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098992
098992
098892, P79904,
01-FEB-1997 (TREMBLREL. 02, CREATED)
01-FEB-1997 (TREMBLREL. 02, LAST SEQUATED)
                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                MX2 PROTEIN.
SALMO SALAR (ATLANTIC SALMON).
     70640 MW;
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Best Local Similarity 71.4%;
Matches 5; Conservative
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Best Local Similarity 71.4%;
5; Conservative
                                    83.7%;
Similarity 71.4%;
5; Conservative
                                                                                                                                                                                                                          PRELIMINARY;
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                                         Query Match
Best Local Similarity
     621 AA;
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MEDLINE: 9732365.

MEDLINE: 9732365.

TROBRIDGE G.D., CHICUD P.D., LEONG J.C.;

"Cloning of the rainbow trout (Oncorhynchus mykiss) Mx2 and Mx3 cDNAs and characterization of trout Mx protein expression in salmon cells."

J. VIROL. 71:5304-5311(1997).

EMBL: 047945; G1399452; -..

EMBL: 047945; G1399452; -..

PROSITE: PROGNANTW; 1.

PROMITE: PROGNANTW; 1.

PRAM: PF00350; dynamin. 1.

PFAM: PF01031; dynamin. 2: 1:

SEQUENCE 635 AA; 72112 MW; 4015A5A9 CRC32;
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                                                                                                                                                                                                                                      Score 41; DB 13; Length 635;
Pred. No. 2.70e+01;
1; Mismatches 1; Indels
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Best Local Similarity 71.4%;
Matches 5; Conservative
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Oct 28 11:33:40 1999; MasPar time 3.26 Seconds 45.628 Million cell updates/sec Run on:

not generated Tabular output

>US-09-081-707-12 (1-7) from US09081707.pep 48

1 ENKISYQ 7 Title: Description: Perfect Score: Sequence:

170751 seqs, 21266608 residues PAM 150 Gap 15 Searched:

Scoring table:

Minimum Match 0% . Listing first 45 summaries Post-processing:

Database:

a-geneseq35

Variance 35.751; scale 0.413 Mean 14.768; Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

					CHILDRINES		
		æ					
Result No.	Score	Query	Query Match Length DB	DB	QI.	Description	Pred No.
:				1			
7	47	97.9	17	17	R89602	Prostate specific ant	2.19e+01
7	47	97.9	17	56	W33439	Oligopeptide 19 cleav	2.19e+01
m	45	93.8	287	32	W51096	Ehrlichia canis VSA1	4.06e+01
4	42	87.5	7	17	R89612	Prostate specific ant	1.01e+02
Ŋ	42	87.5	7	56	W33449	Oligopeptide 29 cleav	1.01e+02
9	42	87.5	ω	56	W33546	Oligopeptide 126 base	1.01e+02
7	42	87.5	∞	26	W33435	Oligopeptide 15 cleav	1.01e+02
ω	42	87.5	σο	17	R89598	Prostate specific ant	1.01e+02
σ	42	87.5	œ	17	R89712	Prostate specific ant	1.01e+02
10	42	87.5	6	11	R89599	Prostate specific ant	1.01e+02
11	42	87.5	σ	17	R89718	Prostate specific ant	1.01e+02
12	42	87.5	9	56	W33552	Oligopeptide 132 base	1.01e+02
13	42	87.5		56	W33488	Oligopeptide 68 cleav	1.01e+02
14	42	87.5	10	26	W33448	Oligopeptide 28 cleav	1.01e+02
15	42	87.5	10	56	W33429	Oligopeptide 9 cleave	1.01e+02
16	42	87.5	10	26	W33463	Oligopeptide 43 cleav	1.01e+02

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Gaps

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Score 47; DB 17; Length 17; Pred. No. 2.19e+01; 1; Mismatches 0; Indels

Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative

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L1112222222222222222222222222222222222	5437

#### ALIGNMENTS

B O D D D D D D D D D D D D D D D D D D	R89602 standard; peptide; 17 AA.  R89602 standsolver antigen, semenogelin derived, cleavage substrate.  Prostate specific antigen, prostate specific antigen; proteolysis; gell structure; dissolution; prostate specific antigen; proteolysis; chymotrypsin like specificity; peptide substrate; cleavage site; assay; determination; proteolytic activity; identification; inhibitor: cytotoxic agent; conjugated; treatment; prostate cancer.  WOSGO0503-A1.  11-JAN-1995; US-267092.  WERL) MERCK & CO INC.  DeFeo-Jones D, Feng D, Garsky VM, Jones RE, Oliff AI:  WFI: 96-077275/08.  New peptide substrates cleaved by prostate cancer, and assay for determination of PSA activity English.  Disclosure: page 60: 142pp; English.  Human semenogelin I (ASD) is one of the major proteins, including hSII and fibronectin, in the sperm entrapping gel formed at election of prostate specific antigen (PSA), a protease with
3555555558	chymotrypsin like specificity, which proteolyses the above major proteins. New substrates, including the present peptide, cleaved by PSA, i.e. peptides contg. a NSI PSA cleavage site, can be used in assays to determine the proteolytic activity of free PSA in a sample, and to identify cpds. which inhibit the proteolytic activity of pSA, they may also be conjugated, via a covalent bond or peptide linker, to a cytotoxic agent and used to treat prostate cancer.  Sequence 17 AA;

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214 qnkisyq 220
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6
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δλ
                                                                                                                                                                                                                                                                                                                                             The present sequence is a novel oligopeptide that is recognised and cleaved by free prostate specific antigen - useful in assays for active antigen, and in oligopeptide-dug conjugates for prostatic cancer treatment bisclosure; Page 81; 192pp; English.

The present sequence is a novel oligopeptide that is recognised and controlled by the prostate specific antigen (PSA). It was designed based on the sequences surrounding the PSA cleavage sites of Semenogelin I, a major sperm entrapping gel protein. PSA, which has confynctypsin-like specificity is responsible for dissolution of the gel structure formed at ejaculation by proteolysis of the major gel proteins (Semenogelin I and II, and fibronectin). Liquefaction of the ejaculate colleases progressively motile spermatozoa. PSA complexed to alpha 1-antichymotrypsin is the predominant form of serum PSA. Serum measurements of PSA are useful for monitoring treatment of adenocarcinom of the prostate. Prostate metastases are also known to secrete immunologically reactive PSA since serum PSA is detectable at high levels in prostatectomised patients showing widespread metastatic prostate concer. Cytotoxic compounds that could be activated by the proteolytic cancer. Cytotoxic compounds that could be activated by the prostate compounds and this oligopeptide are useful in treatment of prostate cancer. The colloppeptide can also be useful in a quantitative assay for enzymatically advantages.
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                                                                                                                27-MAR-1998 (first entry) Oligopeptide 19 cleaved by free prostate specific antigen. Oligopeptide 19 cleaved by free prostate specific antigen, poligopeptide, proteolytic cleavage; prostate specific antigen; PSA; cleavage site; Semenogelin I; chymotrypsin-like; serum PSA; adenocarcinoma; prostate metastases; prostate cancer; treatment; detection; cytotoxic conjugate; activation; quantitative assay.
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Ehrlichia canis VSA1 protein (partial sequence).
MAP1 homologue; variable surface antigen; VSA1; rickettsia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 47; DB 26; Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 2.19e+01;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                         DeFeo-Jones D, Feng D, Garsky VM, Jones RE, Oliff AI;
                                                                                                                                                                                                                                      /note= "PSA specific cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "putative signal peptide"
                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .T 3
W51096 standard; Protein; 287 AA.
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W33439 standard; Peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.9%;
Similarity 85.7%;
6; Conservative
                                                                                                                                                                                                                                                                           02-OCT-1996; U15713.
06-OCT-1995; US-540412.
(MERI ) MERCK & CO INC.
                                                                                                                                                                                                                                                                                                                                   WPI; 97-225974/20.
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       dnkisyq 9
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ENKISYQ 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   active PSA.
                                                                                                                                                                                                                                                                    10-APR-1997
                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                      W33439;
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This is the full length variable surface antigen VSA1 protein of Ehrlichia canis. Its amino acid sequence was deduced from open reading frame (ORF) 10 f a genomic locus (see VOT180) of E. canis that was obtained on the basis of homology to the major antigenic protein MAP1 (see W51088) of Cowdria ruminantium. This genomic cours included 2 ORFs encoding similar, but non-identical proteins (see W51096-97). A claimed composition comprises a nucleic acid see VOT176-82) encoding a polypeptide (see W51089-99) that elicits a protective immune response against a rickettsial pathogen. The nucleic acid is used, in human or veterinary medicine, in vaccines to protect against Rickettsial, Ehrlichia. Anaplasma and Cowdria species. The Ehrlichia antigenic polypeptides can be used diagnostically to detect antibodies associated with Ehrlichia infection (claimed). Sequence 287 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The peptide substrates cleaved by prostate-specific antigen - also cytotoxic conjugates for treating prostate cancer, and assay for determination of PSA activity.

The determination of PSA activity.

Claim 6: Page 64; 142pp; English.

Human semenogelin I (hSI) is one of the major proteins, including the major proteins, including the sperm entrapping gel formed at ejaculation. This gel structure undergoes dissolution via the ejaculation. This specific antigen (PSA), a protease with action of prostate specificity, which proteolyses the above major proteins. New substrates, including the prosent peptide, cleaved by PSA, i.e. peptides contg. a hSI PSA cleavage site, can be used in assays to determine the proteolytic activity of free PSA in a sample, and to identify cgds. Which inhibit the proteolytic activity of PSA, they may also be conjugated, via a covalent bond
                                                                                                                                                                                                                                                                                           useful for, e.g. stimulating protective immune response in humans or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prostate specific antigen, semenogelin derived, cleavage substrate. Human; semenogelin I; sperm entrapping gel; ejaculation; protease; gel structure; dissolution; prostate specific antigen; proteolysis; chymotrypsin like specificity; peptide substrate; cleavage site; assay; determination; proteolytic activity; identification; inhibitor; cytotoxic agent; conjugated; treatment; prostate cancer. Homo sapiens.
                                                                                                                                                                                                                                                  Composition containing nucleic acid encoding rickettsial antigen
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Pred. No. 4.06e+01;
1; Mismatches 0; Indels
                                                                                          Ganta RR, Mahan SM, McGuire TC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Garsky VM,
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R89612 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                animals
Claim 3; Fig 2C; 39pp; English.
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85.7%;
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15-WAR-1995; US-404833.
(MERI ) MRECK & CO INC.
DeFCO-JONES D, Feng D,
WPI; 96-077275/08.
17-0CT-1996; US-733230.
(UYFL) UNIV FLORIDA.
Barbet AF, Burridge MJ,
Nyika A, Rurangirwa FR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-JAN-1996.
07-JUN-1995; U08156.
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Best Local Similarity
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10-APR-1997.
02-OCT-1996; U15713.
06-OCT-1995; US-540412.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oligopeptide-drug conjugates for active antigen, and in oligopeptide-drug conjugates for prostatic cancer treatment oligopeptide-drug conjugates for prostatic cancer treatment clients is a novel oligopeptide that is recognised and protein Psecent sequence is a novel oligopeptide that is recognised and protein Psecent sequence is a novel oligopeptide that is recognised and protein Psecent sequences surrounding the PsA cleavage sites of centrally cleaved by free prostate specificity is responsible for dissolution of the gel structure formed at ejaculation by proteolysis of the major gel proteins comported in and II, and fibronectin). Liquefaction of the ejaculate releases progressively motile spermatozoa. PSA complexed to alpha 1-antichymotrypsin is the predominant form of serum PSA. Serum measurements of PSA are useful for monitoring treatment of adenocarcinoma of the prostate. Prostate metastases are also known to secrete immunologically reactive PSA since serum PSA is detectable at high levels in prostatectomised patients showing widespread metastatic prostate cancer. Cytotoxic compounds that could be activated by the proteolytic carivity of PSA should also be prostate cell specific as well as specific or activity of PSA should also be prostate cell specific as well as specific or and this oligopeptide are useful in treatment of prostate cancer. The colligopetide can also be used in a quantitative assay for enzymatically
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                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-MAR-1998 (first entry)
Oligopeptide 29 cleaved by free prostate specific antigen.
Oligopeptide, proteolytic cleavage; prostate specific antigen; PSA;
cleavage site; Semenogelin I; chymotrypsin-like; serum PSA;
adenocarcinoma; prostate metastases; prostate cancer; treatment;
detection; cytotoxic conjugate; activation; quantitative assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Oligopeptide 126 based on Semenogelin I cleavage site.
Oligopeptide; proteolytic cleavage; prostate specific antigen; PSA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oligopeptide(s) recognised and cleaved by free prostate specific antigen - useful in assays for active antigen, and in
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   to a cytotoxic agent and used to treat
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Pred. No. 1.01e+02;
0; Mismatches 0; Indels
                                                                                                                              Score 42; DB 17; Length 7;
Pred. No. 1.01e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DeFeo-Jones D, Feng D, Garsky VM, Jones RE, Oliff AI, WPI; 97-225974/20.
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/note= "PSA specific cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LT 6
W33546 standard; Peptide; 8 AA.
W33546;
                                                                                                                                                                                                                                                                                                                                                                                                                           JT 5
W33449 standard; Peptide; 7 AA.
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Best Local Similarity 100.08;
                                                                                                                              Query Match
Best Local Similarity 100.0%;
                                                                                                                                                                                                6; Conservative
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06-OCT-1995; US-540412.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MERI ) MERCK & CO INC
peptide linker,
                              prostate cancer.
Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 AA:
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                                                                                                                                  Query Match
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8 666
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antigen - useful in assays for active antigen, and in clayer. It is a serial in assays for active antigen, and in clayer. In a state of the prostatic cancer treatment ps claim 3; page 160; 192p; English.

The present sequence is a novel oligopeptide designed based on the sequences surrounding the prostate special cantigen (PSA) cleavage sites of Semenogelin I, a major sperm entrapping gel protein. PSA, which has conformed at ejaculation by proteolysis of the major gel proteins of the major gel protein of the gel structure formed at ejaculation by proteolysis of the major gel proteins of scructure formed at ejaculation by proteolysis of the major gel proteins of semenogelin I and II, and fibronectin). Liquefaction of the ejaculate of alpha 1-antichymotrypsin is the predominant form of serum PSA. Serum measurements of PSA are useful for monitoring treatment of adenocarcinoma of the prostate. Prostate metastases are also known to secrete immunologically reactive PSA since serum PSA is detectable at high levels of in prostatectomised patients showing widespread metastatic prostate cancer. Cytotoxic compounds that could be activated by the proteolytic activity of PSA secreting prostate metastases. Conjugates of cytotoxic compounds and this oligopeptide are useful in treatment of prostate cancer. The oligopeptide can also be used in a quantitative assay for enzymatically
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Oligopeptide 15 cleaved by free prostate specific antigen.
Oligopeptide, proteolytic cleavage, prostate specific antigen; PSA,
Cleavage site; Semenogelin I; chymotrypsin-like; serum PSA,
adenocarcinoma, prostate metastases, prostate cancer; treatment,
detection; cytotoxic conjugate; activation; quantitative assay.
cleavage site; Semenogelin I; chymotrypsin-like; serum PSA; adenocarcinoma; prostate metastases; prostate cancer; treatment; detection; cytotoxic conjugate; activation; quantitative assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligopeptide(s) recognised and cleaved by free prostate specific antigen - useful in assays for active antigen, and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "optionally N-terminally acetylated, when C-terminally amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DeFec-Jones D, Feng D, Garsky VM, Jones RE, Oliff AI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "PSA specific cleavage site"
                                                                                                                                                                                                                                                 /note= "PSA specific cleavage site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                      Location/Qualifiers
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Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                   06-OCT-1995; US-540412.
(MERI ) MERCK & CO INC.
                                                                                                                                                                                                                                                                                                                           10-APR-1997.
02-OCT-1996; U15713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 97-225974/20.
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DeFeo-Jones D, Fe
WPI; 96-077275/08.
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Sequence 8 AA)
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                                                         The properties of the prostate specific antigen - useful in assays for active antigen, and in assays for active antigen, and in assays for active antigen, and in a say for active antigen, and in a says for active antigen, and in a say for active antigen, and in a conjugates for prostatic cancer treatment antigen - useful in assays for prostatic cancer treatment conjugates for proteolytically cleaved by free prostate specific antigen (PSA). It was designed based on the sequences surrounding the PSA cleavage sites of Semenogelin I, a major sperm entrapping gel protein. PSA, which has chymotrypsin-like specificity is responsible for dissolution of the gel structure formed at ejaculation by proteolysis of the major gel proteins (Semenogelin I and II, and fibronectin). Liquefaction of the ejaculate conference formed at ejaculation by proteolysis of the major genum PSA. Serum Conference of PSA are useful for monitoring treatment of adenocarcinoma (The prostate. Prostate metastases are also known to secrete immunologically reactive PSA since serum PSA is detectable at high levels of prostate conjugates of cytotoxic compounds that could be activated by the proteolytic cancer. Cytotoxic compounds that could be activated by the proteolytic concer. Cytotoxic compounds that could be activated by the proteolytic and this oligopeptide are useful in treatment of prostate cancer. The oligopeptide can also be used in a quantitative assay for enzymatically could per second adjected with an active proved. Cytotoxic compounds and a C-terminal amide group) was digested with anzymatically active PSA. After four hours 30 per cent of the peptide salt was cleaved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Prostate specific antigen, semenogelin derived, cleavage substrate.
Human, semenogelin I: sperm entrapping gel; ejaculation; protease;
gel structure; dissolution; prostate specific antigen; proteolysis;
enmotrypain like specificity; peptide substrate; cleavage site;
assay; determination; proteolytic activity; identification;
inhibitor; cytotoxic agent; conjugated; treatment; prostate cancer.
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Claim 3: Page 58: 142pp: English.

Human semenogelin I (ASI) is one of the major proteins, including hSII and fibronectin, in the sperm entrapping gel formed at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Garsky VM, Jones RE, Oliff AI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42; DB 26; Length 8;
Pred. No. 1.01e+02;
0; Mismatches 0; Indels
                          Feng D, Garsky VM, Jones RE, Oliff AI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "opt. acylated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.0%;
Matches 6: Concount
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15-MAR-1995; US-404833.
(MERI ) MERCK & CO INC.
DeFeo-Jones D, Feng D,
WPI; 96-077275/08.
(MERI ) MERCK & CO INC.
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07-JUN-1995; U08156.
                       Defeo-Jones D, Fen
WPI; 97-225974/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 nkisyg 6
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2 NKISYQ 7
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Claim 3: Page 108: 142pp: English.

Human semenogelin I (hSI) is one of the major proteins, including than semenogelin I (hSI) is one of the major proteins, including claculation. This gel structure undergoes dissolution via the ejaculation. This gel structure undergoes dissolution via the action of prostate specific antigen (PSA), a protease with action of prostate specific antigen (PSA), a protease with cromotrypsin like specificity, which proteolyses the above major proteins. New substrates, including the present peptide, cleaved by PSA, i.e. peptides contg. a hSI PSA cleavage site, can be used in assays to determine the proteolytic activity of free PSA in a sample, and to identify odes. Which inhibit the proteolytic activity of pSA, they may also be conjugated, via a covalent bond or peptide linker, to a cytotoxic agent and used to treat
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ejaculation. This gel structure undergoes dissolution via the action of prostate specific antigen (PSA), a protease with chymotrypsin like specificity, which proteolyses the above major proteins. New substrates, including the present peptide, cleaved by PSA, i.e. peptides contg. a hSI PSA cleavage site, can be used in assays to determine the proteolytic activity of free PSA in a sample, and to identify cpds. which inhibit the proteolytic activity of PSA, they may also be conjugated, via a covalent bond or peptide linker, to a cytotoxic agent and used to treat prostate cancer. In a PSA hydrolysis assay, the percentage of the present peptide cleaved by YORK PSA after 4 hrs. was 30 % acylated and amidated.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 42; DB 17; Length 8; Pred. No. 1.01e+02; 0; Mismatches 0; Indels
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Pred. No. 1.01e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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R89712 standard; peptide; 8 AA.
R89712;
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Best Local Similarity 100.0%;
Matches 6; Conservative
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Best Local Similarity 100.0%;
Matches 6; Conservative
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15-MAR-1995; US-404833.
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07-JUN-1995; U08156.
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                                           Prostate specific antigen, semenogelin derived, cleavage substrate. Human; semenogelin I; sperm entrapping gel; ejaculation; protease; gel structure; dissolution; prostate specific antigen; proteolysis; chymotrypsin like specificity; peptide substrate; cleavage site; assay; determination; proteolytic activity; identification; inhibitor; cytotoxic agent; conjugated; treatment; prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human: semenogelin I; sperm entrapping gel; ejaculation; protease; gel structure; dissolution; prostate specific antigen; proteolysis; chymotrypsin like specificity; peptide substrate; cleavage site; assay; determination; proteolytic activity; identification; inhibitor; cytotoxic agent; conjugated; treatment; prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-SEP-1996 (first entry)
Prostate specific antigen, semenogelin derived, cleavage substrate.
                                                                                                                                                                                                                                                                                           New peptide substrates cleaved by prostate-specific antigen - also cytotoxic conjugates for treating prostate cancer, and assay for determination of PgA activity.

Claim 3; Page 58; 142pp; English.

Human semenogelin I (AIS) is one of the major proteins, including hSI and fibronectin, in the sperm entrapping gel formed at ejaculation. This gel structure undergoes dissolution via the
                                                                                                                                                                                                                                                                                                                                                                                     action of prostate specific antigen (PSA), a protease with chymotrypsin like specificity, which proteolyses the above major proteins. New substrates, including the present peptide, cleaved by PSA, i.e. peptides contg. a hSI PSA cleavage site, can be used in assays to determine the proteolytic activity of free PSA in a activity of free PSA in a activity of PSA, they may also be conjugated, via a covalent bond or peptide linker, to a cytotoxic agent and used to treat
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                                                                                                                                                              /note= "prostate specific antigen proteolytic cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prostate cancer. In a PSA hydrolysis assay, the percentage of the present peptide cleaved by YORK PSA after 4 hrs. was 55 %
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "prostate specific antigen proteolytic
                                                                                                                                                                                                                                                                    Garsky VM, Jones RE, Oliff AI;
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Pred. No. 1.01e+02;
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                                                                                                                                     Location/Qualifiers
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R89718 standard; peptide; 9 AA.
         standard; peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cleavage site"
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Best Local Similarity 100.0%;
Matches 6; Conservative
                               02-SEP-1996 (first entry)
                                                                                                                                                                                                  11.JAN-1996.
07-JUN-1995; U08156.
28-UUN-1994; U5-267092.
15-MAR-1995; US-404833.
(MERI ) MERCK & CO INC.
DeFCO-JONES D, Feng D, CWPI; 96-077275/08.
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28-JUN-1994; US-267092.
15-MAR-1995; US-404833.
(MERI ) MERCK & CO INC.
DeFeo-Jones D, Feng D, (
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      R89599 s
R89599;
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The present sequence is a novel oligopeptide designed based on the sequences surrounding the prostate specific antigen (PSA) cleavage sites of Semenogelin I, a manjor sperm entrapping gel protein. PSA, which has chymnotrypsin-like specificity is responsible for dissolution of the gel structure formed at ejaculation by proteolysis of the major gel proteins (Semenogelin I and II, and fibronectin). Liquefaction of the ejaculate releases progressively motile spermatozoa. PSA complexed to alpha 1-antichymotrypsin is the predominant form of serum PSA. Serum measurements of PSA are useful for monitoring treatment of adenocarcinoma of the prostate. Prostate metastases are also known to secrete immunologically reactive PSA since serum PSA is detectable at high levels in prostatectomised patients showing widespread metastatic prostate cancer. Cytotoxic compounds that could be activated by the proteolytic activity of PSA should also be prostate cell specific as well as specific confounds that could be activated by the proteolytic cativity of PSA should also be prostate cell specific as well as specific confounds.
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New peptide substrates cleaved by prostate-specific antigen - also cytotoxic conjugates for treating prostate cancer, and assay for determination of PSA activity.

T determination of PSA activity.

Claim 4: Page III; 142pp: English.

Human semenogelin I (hSI) is one of the major proteins, including hSII and fibronectin, in the sperm entrapping gel formed at ection of prostate specific antigen (PSA), a protease with action of prostate specific antigen (PSA), a protease with chymotrypsin like specificity, which proteolyses the above major cymotrypsin like specificity, which proteolytic activity of free PSA in a says to determine the proteolytic activity of free PSA in a continity, and the proteolytic sample, and to identify cyds, which inhibit the proteolytic activity of sample.
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Oligopeptide, proteolytic cleavage; prostate specific antigen; PSA; cleavage site; Semenogelin I; chymotrypsin-like; serum PSA; adenocarcinoma; prostate metastases; prostate cancer; treatment; detection; cytotoxic conjugate; activation; quantitative assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activity of PSA, they may also be conjugated, via a covalent bond or peptide linker, to a cytotoxic agent and used to treat
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Claim 4; Page 161; 192pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 42; DB 17; Length 9;
Pred. No. 1.01e+02;
0; Mismatches 0; Indels
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WPI; 97-225974/20.
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/note= "PSA specific cleavage site"
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W33552 standard; Peptide; 9 AA.
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Best Local Similarity 100.0%;
Matches 6; Conservative
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02-OCT-1996; U15713.
06-OCT-1995; US-5404
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Length 9;

DB 26;

Score 42;

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Synthetic.
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Oligopeptide(s) recognised and cleaved by free prostate specific reduction useful in assays for active antigen, and in antigen - useful in assays for active antigen, and in proligopeptide-fug conjugates for prostatic cancer treatment bisclosure: Page 102: 192pp; English.

Crossing proteolytically cleaved by free prostate specific antigen (PSA). It was considered based on the sequences surrounding the PSA cleavage sites of semenogalin I, a major sperm entrapping gel protein. PSA, which has computing specificity is responsible for dissolution of the gel structure formed at ejaculation by proteolysis of the major gel proteins of the major specificity is responsible for dissolution of the gel structure formed at ejaculation by proteolysis of the major gel proteins of semenogalin I and II, and fibronectin). Liquefaction of the ejaculate crossively motile spermatozoa. PSA complexed to alpha 1-antichymotrypsin is the predominant form of serum PSA. Serum measurements of PSA are useful for monitoring treatment of adenocarcinoma of the prostate. Prostate metastases are also known to secrete communication prostate compounds that could be activated by the proteolytic cancer. Cytotoxic compounds that could be activated by the proteolytic cancer. Cytotoxic compounds that could be activated by the proteolytic compounds also be prostate cell specific as well as specific control of prostate can also be useful in treatment of prostate cancer. The coligopeptide are useful in treatment of prostate cancer. The coligopeptide was digested with enzymatically active PSA. After 4 hours 39 conserved to a ba.
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                                                                                                                                                                       27-MAR-1998 (first entry)
Oligopeptide 68 cleaved by free prostate specific antigen.
Oligopeptide, proteolytic cleavage; prostate specific antigen; PSA; cleavage site; Semenogelin I; chymotrypsin-like; serum PSA; adenocarcinoma; prostate metastases; prostate cancer; treatment; detection; cytotoxic conjugate; activation; quantitative assay.
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                                                                                                                                                                                                                                                                                                         /note= "PSA specific cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 1.01e+02;
                                                                                                                                                                                                                                                                              Location/Qualifiers
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W33448 standard; Peptide; 10 AA.
                                                                                                                                              W33488 standard; Peptide; 9 AA.
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Best Local Similarity 100.0%;
Matches 6; Conservative
             Best Local Similarity 100.0%;
                             Conservative
                                                                                                                                                                                                                                                                                                                                            10-AFK-1997.
02-OCT-1996; U15713.
06-OCT-1995; US-540412.
(MERI ) MERCK & CO INC.
                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 97-225974/20.
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                                                          nkisyg 7
                                                                                   2 NKISYQ 7
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The present sequence is a novel oligopeptide that is recognised and proteolytically cleaved by free prostate specific antigen (PSA). It was designed based on the sequences surrounding the PSA cleavage sites of Semenogelin I, a major sperm entrapping gel protein. PSA, which has common specificity is responsible for dissolution of the gel structure formed at ejaculation by proteolysis of the major gel proteins (Semenogelin II, and fibronectin). Liquefaction of the ejaculate of Semenogelin I and II, and fibronectin). Liquefaction of the ejaculate of servences progressively motile spermatozoa. PSA complexed to alpha 1-antichymotrypsin is the predominant form of serum PSA. Serum of the prostate. Prostate metastasss are also known to secrete immunologically reactive PSA since serum PSA is detectable at high levels in prostatectonised patients showing widespread metastatic prostate cancer. Cytotoxic compounds that could be activated by the proteolytic activity of PSA should also be prostate cell specific as well as specific of PSA secreting prostate metastases. Conjugates of cytotoxic compounds and this oligopeptide are useful in treatment of prostate cancer. The oligopeptide can also be used in a quantitative assay for enzymatically
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oligoperide(s) recognised and cleaved by free prostate specific antigen. useful in assays for active antigen, and in oligopeptide-drug conjugates for prostatic cancer treatment claim 4 and 17; Page 161: 192pp; English.
                                                                                                                                                                                                                                                                                                                                                           Oligopeptide(s) recognised and cleaved by free prostate specific antigen - useful in assays for active antigen, and in oligopeptide drug conjugates for prostatic cancer treatment claim 6; Page 162; 192pp; English.
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Pred. No. 1.01e+02;
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/note= "PSA specific cleavage site"
                                                                        /note= "PSA specific cleavage site"
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W33429 standard; Peptide; 10 AA.
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                                                                                                                                                                                                                                                            (MERI ) MERCK & CO INC
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02-OCT-1996; U15713.
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WPI; 97-225974/20.
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The present sequence is a novel oligopeptide that is recognised and casined based by free prostate specific antigen (PSA). It was casined based on the sequences surrounding the PSA cleavage sites of Semenogelin I, a major sperm entrapping gel protein. PSA, which has chymotrypsin-like specificity is responsible for dissolution of the gel structure formed at ejaculation by proteolysis of the major gel proteins of structure formed at ejaculation by proteolysis of the major gel proteins (Semenogelin I and II, and fibronectin). Liquedaction of the ejaculate releases progressively motile spermatozoa. PSA complexed to alpha 1-antichymotrypsin is the predominant form of serum PSA. Serum measurements of PSA are useful for monitoring treatment of adenocarcinoma of the prostate. Prostate metastases are also known to secrete immunologically reactive PSA since serum PSA is detectable at high levels in prostatectomised patients showing widespread metastatic prostate cancer. Cytotoxic compounds that conjugates of cytotoxic compounds confinity of PSA should also be prostate cell specific as well as specific a confit is oligopeptide can also be useful in treatment of prostate cancer. The oligopeptide can also be used in a quantitative assay for enzymatically cartive PSA. In a study of cleavage affinity, the TFA salt of this peptide was algested with enzymatically active PSA. After four hours 62 per cent of the peptide was cleaved.
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Search completed: Thu Oct 28 11:33:57 1999 Job time : 17 secs.

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0; Gaps

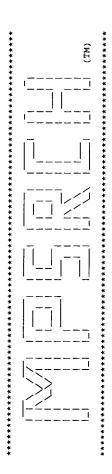
Score 42; DB 26; Length 10; Pred. No. 1.01e+02; 0; Mismatches 0; Indels

Query Match 87.5%; Best Local Similarity 100.0%; Matches 6; Conservative

1 nkisyg 6 ||||||| 2 NKISYQ 7

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Oct 28 11:34:13 1999; MasPar time 2.93 Seconds 95.729 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-081-707-12 (1-7) from US09081707.pep 48 Title: Description: Perfect Score:

1 ENKISYQ 7 Sequence:

122810 segs, 40068593 residues Searched:

PAM 150 Gap 15

Scoring table:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir60 1:pir1 2:pir2 3:pir3 4:pir4

Mean 20.537; Variance 21.176;

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

scale 0.970

# SUMMARIES

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Pred. No.	4.61e-01	2.60e+00	7.90e+00	1.36e+01	1.36e+01	1.36e+01	1.36e+01	1.36e+01	2.31e+01	2.31e+01	2.31e+01	2.31e+01	2.31e+01	3.90e+01	3.90e+01	3.90e+01	3.90e+01	3.90e+01	3.90e+01	6.51e+01	6.51e+01	6.51e+01	6.51e+01
Description	semenogelin II precur	an	DNA topoisomerase (EC		semenogelin I precurs	HE65 protein - Autogr	hypothetical protein			hypothetical protein	phosphopyruvate hydra	probable phenylalanin	carbonic anhydrase II	transcription antiter	hypothetical protein	type III restriction	type III restriction	guanylate cyclase (EC	probable membrane pro	aminoglycoside N6'-ac	ribosomal protein S4	hypothetical protein	fimbrial adhesin F17-
ΙD	A43412	JE0220	E64213	A32885	WTHUB	I49834	S73757	E64576	S28006	D64303	JC4036	S75388	147228	S39702	S75459	A64710	E71810	I59385	S64921	A61158	664323	14	A42359
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Length	582	287	709	384	462	553	879	1021	312	319	439	544	704	276	374	624	696	1108	2958	144	187	287	344
% Query Match	100.0	93.8	9.68	87.5	87.5	87.5	87.5	87.5	85.4	85.4	85.4	85.4	85.4	83.3	83.3		83.3	83.3	83.3	81.3	81.3	81.3	81.3
Score	48	. 45	43	42	42	42	42	42	41	41	41	41	. 41	40	40	40	40	40	40	39	39	39	39
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S29155 Schneider, K.; Kausler, W.; Tripier, D.; Jouvenal, K.; Spiteller, G. Biol. Chem. Hoppe-Seyler (1989) 370:353-356 Isolation and structure determination of two peptides

#accession A45295 ##molecule\_type mRNA ##residues 3-582 ##label LI2 ##cross-references GB:M81652

#authors #journal

REFERENCE

3 379 2 S57952 3 347 2 B64696 3 420 2 S43559 43 420 2 S43559 43 434 2 A57886 3 484 2 E75068 484 2 E71061 3 609 2 S67016 3 609 2 F71821 3 1062 2 F71821 3 1087 2 E71821 3 1087 2 E71821 3 1087 2 E71821 3 1087 2 E71821 3 1089 2 G7016 3 1234 2 B36186 3 1234 2 B36186 3 1234 2 G70163 3 2 G70163 5 544 2 GC5503 2 178 2 S5805	ALIGNMENTS  ALIGNMENTS  AM3412 #type complete semenogelin II precursor - human #formal_name Homo sapiens #common_name man 30-Sep1993 #sequence_revision 30-Sep-1993 #text_change 22-May-1998 AM3412: B31489; A45295; S29156; S68765; S68762 AM3412: B31489; A45295; S29156; S68765; S68762 AM3412: B11489; A45295; S29156; S68765; S68762 AM3412: Districture of semenogelin I and II. The predominant proteins in human semen are encoded by two homologous genes on chromosome 20 erences MUID:92388176 AM3412 Ule_4Type DNA uss carracted from NCBI Dackbone (NCBIN:112887, NCBIP:112889) Lilja, H.; Abrahamsson, P.A.; Lundwall, A. Teferences GB:M81651; NID:9307417; PID:9307418 Sequence extracted from NCBI Dackbone (NCBIN:112887, NCBIP:112889) Lilja, H.; Abrahamsson, P.A.; Lundwall, A. The male accessory sex glands and on the spermatozoa. B31489 Structure and identification of closely related proteins in the male accessory sex glands and on the spermatozoa. B31489 Suncleic acid sequence not shown use 214-278, Y', 280-281 ##label LIL AA5295 FOOTO NAIL Acad. Sci. U.S.A. (1992) 89:4559-4563 Modecular cloning of epididymal and seminal vestcular ranscripts encoding a semenogelin-related protein.  Franscripts encoding a semenogelin-related protein.  Franscripts mcNail Sci. U.S.A. (1992) 89:4559-4563 A45295 A5526479
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2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	RESULT  ENTRY  TITLE  ORGANISM  DATE  ACCESSIONS  REFERENCE  # fournal  # file  # residues  # mote  REFERENCE # authors - refere  # accession  # file  # residues  # fournal  # file  # residues  # fournal  # file  # cross - refere  # authors - refere  # accession  # file  # residues  # fournal  # title  # cross - refere  # accession  # # residues  # file  # residues  # file  # residues  # residues  # residues  # recossion  # # residues  # residues

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Best Local Similarity 85.7%; Pred. No. 2.60e+00; Matches 6; Conservative 1; Mismatches 0;
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KEYWORDS isom
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                                                                                                        this report is of a secondary sequence determined simultaneously with the sequence with accession number $29155 (see entry WTHUB); as a secondary sequence, it should be considered less than fully reliable
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Isolation and characterization of the major gel proteins in
human semen, semenogelin I and semenogelin II.
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Burridge, M.J.; Alleman, A.R.
#journal Biochem. Biophys. Res. Commun. (1998) 247:636-643
#title Molecular characterization of a 28kDa surface antigen gene family of the tribe Bhrlichiae.
#cross-references_MUID:98321180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #domain signal sequence #status predicted #label SIG\
#product semenogelin II #status predicted #label MAT\
#binding_site carbohydrate (Asn) (covalent) #status
                                           ##molecule_type protein
##residues 390,'E',392-396,'E',398-400,'EW',403-405,'C',407,'DE'
##label SCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *superfamily semenogelin duplication; glycoprotein; semen; seminal vesicle; tandem
                                                                                                                                                                                                           Kise, H.; Nishioka, J.; Kawamura, J.; Suzuki, K.
Bur. J. Blochem. (1996) 238:88-96
Characterization of semenogelin II and its molecular
interaction with prostate-specific antigen and protein
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28k surface antigen 1 - Ehrlichia canis
#formal_name Ehrlichia canis
21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change
17-Mar-1999
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Y #length 287 #molecular-weight 32014 #checksum 463
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Pred. No. 4.61e-01;
0; Mismatches 0; Indels
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##residues 420-421,'G',423-423 ##label MAL
occurring in human seminal plasma $29156
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#map_position 20q12-20q13.1
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#accession JEULZL
##molecule_type DNA
##molecule_type TAR ##label RED
1-287 ##label RED
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#accession S68765
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Best Local Similarity 100.0%;
Matches 7; Conservative
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#authors Kreuzer, P.; Gaertner, D.; Allmansberger, R.; Hillen, W.
#journal J. Bacteriol. (1989) 171:3840-3845
#title Identification and sequence analysis of the Bacillus subtilis
#cross-references MID:89291732
#accession A32885
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Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.;
Bolotin, A.; Borchert, S.; Boriss, R.; Boursier, L.; Brans,
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#journal Science (1995) 270:397-403
#title
#cross-references MUID:96026346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##Tresidues
##cross-references GB:U39691; GB:L43967; NID:g1045794; PID:g1045802;
TIGR:MG122
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Gaps
                                                                                                                                                                                                                                                                                              type I DNA topoisomerase
#formal_name Mycoplasma genitalium
17.Nov-1995 #sequence_revision 17.Nov-1995 #text_change
10.oct-1997
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DNA topoisomerase (EC 5.99.1.2) - Mycoplasma genitalium
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##cross-references GB:M27248; NID:g143840; PID:g143841
##experimental_source strain W23
##authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     preliminary; nucleic acid sequence translation not shown
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#length 709 #molecular-weight 82544
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Pred. No. 7.90e+00;
2; Mismatches 0
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Similarity 71.4%;
5; Conservative
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##molecule_type DNA
##residues 1-38
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B43412; A31489; A91335; S29155; A43500; A91320; S29380;
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A.; Braun, M.; Brignell, S.C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi. S.K.; Coddani, J.J.; Connerton, I.F.; Cummings, N.J.; Daniel, R.A.; Denizot, F.; Devine, K.M.; Duesterhoeft, A.; Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita, Y.; Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita, S.Y.; Fujita, Y.; Funis, S.; Galazzi, A.; Gallacn, N.; Ghim, S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandi, G.; Giseph, G.; Guy, B.J.; Haga, K.; Halech, J.; Harwood, C.R.; Henaut, A.; Hibert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.; Kasahara, Y.; Kaerr-Blanchard, M.; Klogh, S.; Kumano, M.; Leazarevit, V.; Lee, S.M.; Levine, S.; Lauber, J.; Rusch, C.; Medjue, C.; Medjue, C.; Medjue, C.; Medjue, N.; Mellado, R.P.; Mizuno, M.; Moestl, D.; Nakai, S.; Noback, M.; Noone, D.; O Reilly, V.; Pooll, T.M.; Portetelle, D.; Porwolik, S.; Rieger, M.; Rapoport, G.; Roche, B.; Rose, M.; Sadaie, Y.; Stot, T.; Scalon, E.; Schleich, S.; Schroeter, R.; Scoffone, F.; Scklyuchi, J.; Schoek, B.; Rose, M.; Tamakoshi, H.; Tarkemaru, K.; Takeuchi, M.; Tamakoshi, H.; Tarkemaru, K.; Takeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstrax, P.; Tognoni, A.; Tosato, V.; Wohlado, M.; Wandeler, F.; Wedler, H.; Wandeler, R.; Wedler, H.; Wannete, R.; Wasanotti, A.; Varanoe, H.; Wannete, R.; Wasanotti, A.; Varanoe, R.; Varanoe,
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The complete genome sequence of the Gram-positive bacterium
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##residues 15-53, SM, 56-82, VV, 84-92, NN, 94-103, VV, 105-107, YR'
110-132, O', 134-140, Fr', 142-154, D', 156-173, S',
175-178, Y', 180-181, S', 183-197, L', 199-205, D',
207-210, V', 212-277, L', 279-284, N', 286-320, V',
322-337, N', 339-347, S', 349-362, O', 364-375, D',
377-380, MIT', 384 ##label KUN
##cross-references GB:299113; GB:AL009126; NID:92634090; PID:e1183418;
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04-Dec-1986 #sequence_revision 03-Oct-1995 #text_change
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DNA binding; transcription regulation
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#length 384 #molecular-weight 42295 #checksum
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Pred. No. 1.36e+01;
2; Mismatches 0; Indels
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semenogelin I precursor - human
seminal basic protein
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Best Local Similarity 71.4%;
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#authors Ulysback, M.; Lazure, C.; Lilja, H.; Spurr, N.K.; Rao, V.V.;
#journal Ulysback, M.; Lazure, C.; Lilja, H.; Spurr, N.K.; Rao, V.V.;
#journal J. Biol. Chem. (1992) 267:18080-18084
#title Gene structure of semenogelin I and II. The predominant proteins in human semen are encoded by two homologous genes on chromosome 20.
#cross-references MIID:92388176
                                                                                                                                                                                                                                                                                                                                                                                                                      #authors A31489
#authors Lilja, H.; Abrahamsson, P.A.; Lundwall, A.
#journal J. Biol. Chem. (1989) 264:1894-1900
#title Semenogelin, the predominant protein in human semen. Primary structure and identification of closely related proteins in the male accessory sex glands and on the spermatozoa.
#cross-references MJID:89109215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lilja, H.: Jeppsson, J.O.
FEBS Lett. (1985) 182:181-184
Amino acid sequence of the predominant basic protein in human
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#journal FEBS Lett. (1984) 167:98-102
#title Partial amino acid sequence of a human seminal plasma peptide
#cross-references MUID:84132557
#accession A91320
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Isolation, structure, and synthesis of a human seminal plasma peptide with inhibin-like activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             this sequence represents a naturally occurring fragment
from proteolytic cleavage of semenogelin during
liquefaction of semen
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##residues 316.320,'L',322-344 ##label SCH
##note this sequence represents the amino end of a natura
##note coccurring fragment from proteolytic cleavage of semenogelin during liquefaction of semen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schneider, K.; Kausler, W.; Tripier, D.; Jouvenal, K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spiteller, G.
Biol. Chem. Hoppe-Seyler (1989) 370:353-356
Isolation and structure determination of two peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##molecule_type mRNA
##residues 1-78,'T',80-422,'K',424-462 ##label LIL
##cross-references GB:J04440
                                                                                                                                                                                                                                                                                                                                                            ##residues 1-462 ##label ULV
##cross-references GB:M81650; NID:g307416; PID:g487420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   occurring in human seminal plasma. S29155
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##residues 108-159 ##label LI2
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##residues 108-138 ##label RAM
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##residues 108-138 ##label SEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #cross-references MUID:85127550
#accession A91335
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*accession A43500
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S68761; A03254
                                                                                                                                                                                                                                                                                                                             ##molecule_type DNA
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#type complete
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larity 85.7%; |
Conservative
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larity 71.4%;
Conservative
virus, ACMNPV
                                                           I49834; S35872
                                       26-Feb-1998
                                                                                                                                                                                                                           ##molecule_type mRNA
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Best Local Similarity
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#genetic_code SGC3
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#journal
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                                                                                                                                                                                                                                                                                                              been proven the amidated tripeptide Glp-Glu-Pro-NH2 (where Glp is pyroglutamic acid) is present in human semen, although the sequence reported here is consistent with an amino-terminally extended form derived from semenogalin, the sequence is followed in semenogalin by Trp, which (unlike Gly) probably cannot become the source of an amide moiety; the authors conclude the peptide must be derived from a closely related protein
                                                                                                                                                                                                                      ##molecule_type protein
##residues 373-397 ##label KHA
##residues the authors' suggestion that this peptide is amidated is
##note consistent with radioimmunoassay results but has not
                                                      Khan, 2.; Smyth, D.G.

Eur. J. Biochem. (1993) 212:35-40

Isolation and identification of N-terminally extended forms of 5-oxoprolylglutamylprolinamide (Glp-Glu-Pro-NH(2)), a thyrotropin-releasing-hormone(TRH)-like peptide present in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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This abundant protein from seminal vesicle secretions maintains a gel-like environment for the sperm cells. At ejaculation, kallikrein-like enzymes in prostatic secretions cleave this protein, resulting in liquefaction of the seminal gel and allowing increased sperm motility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eur. J. Biochem. (1996) 238:48-53
Isolation and characterization of the major gel proteins in
human semen, semenogelin I and semenogelin II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Malm, J.; Hellman, J.; Magnusson, H.; Laurell, C.B.; Lilja,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149834 #type complete
HE65 protein - Autographa californica nuclear polyhedrosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #region semenogelin short repeat 1\
#region semenogelin short repeat 2\
#region semenogelin long repeat 1\
#region semenogelin long repeat 2\
#region semenogelin short repeat 3\
#region semenogelin short repeat 3\
#binding_site carbohydrate (Asn) (covalent) #status
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#label MAT\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #formal_name Autographa californica nuclear polyhedrosis
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from proteolytic cleavage of semenogelin during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #disulfide_bonds interchain #status experimental #length 462 #molecular-weight 52117 #checksum 9901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  duplication; glycoprotein; semen; seminal vesicle
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0; Mismatches 0; Indels
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p_position 20q12-20q13.1
                   liquefaction of semen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *superfamily semenogelin
                                                                                                                                                                                   #cross-references MUID:93185635
#accession S29380
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Best Local Similarity 100.0%;
Matches 6; Conservative
                                                                                                                                                                      human semen.
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                                                             #authors
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282-339
342-399
414-455
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hypothetical protein F11_orf879 - Mycoplasma pneumoniae (ATCC 29342) (SGC3)
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                                                                                                     #authors Becker, D.; Knebel-Morsdorf, D.
#journal J. Virol. (1993) 67:5867-5872
#title Sequence and temporal appearance of the early transcribed
baculovirus gene HE65.
#cross-references MUID:93381786
#accession I49834
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hypothetical protein HP0453 - Helicobacter pylori (strain
26695)
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27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change
17-Jul-1998
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09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change
10-Oct-1997
E64576
A64520
04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                 #length 553 #molecular-weight 65576 #checksum 4566
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                                                                                                                                                                                                                                                                                         ##residues 1-553 ##label RES
##cross-references EMBL:X73577; NID:g313679; PID:g313680
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 553;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #journal Nucleic Acids Res. (1996) 24:4420-4449
#title Complete sequence analysis of the genome of Mycoplasma pneumoniae.
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Pred. No. 1.36e+01;
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A64300
Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, J.A.; FitzGerald, L.M.; Clayton, R.A.; Gocayne, J.D.; Kerlavage, A.R.; Dougherty, B.A.; Tomb, J.F.; Adams, M.D.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Scott, J.L.; Geoghagen, N.S.M.; Weidmann, J.F.; Fuhrmann, J.L.; Nquyen, D.; Utterback, T.R.; Kelley, J.M.; Peterson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.; Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.R.; Venter, J.C. Science (1996) 273:1058-1073
Complete genome sequence of the methanogenic archaeon, Methanosccus januaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #superfamily enolase
carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase
#length 439 #molecular-weight 47323 #checksum 4121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##molecule_type mRNA
##molecule_type mRNA
##residues 1-439 ##label JAC
##cross-references GB:U13799; NID:9535441; PID:9535442
##cross-references GB:U13799; NID:9535441; PID:9535442
##note The authors translated the codon GTC for residue 20 as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene (1995) 154:109-113
A cDNA from Schizosaccharomyces pombe encoding a putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##residues
##residues
##cross-references GB:U67461; GB:L77117; NID:g1590827; PID:g1590830;
TIGR:MJ0028; PID:g1510201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JC4036 #type complete
phosphopyruvate hydratase (EC 4.2.1.11) - fission yeast
(Schizosaccharomyces pombe)
2.phospho-D-glycerate hydrolyase; enolase
#formal_name Schizosaccharomyces pombe
13.un-1995 #sequence_revision 14.Jul-1995 #text_change
                                                           #formal_name Methanococcus jannaschii
13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change
10-Oct-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #map_position REV29473-28514 SUMMARY #length 319 #molecular-weight 36160 #checksum 7290
               hypothetical protein HI1305 homolog - Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid sequence not shown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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This glycolytic enzyme catalyzes the dehydration
2-phosphoglycerate to phosphoenolpyruvate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 2.31e+01;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41; DB 2; L. Pred. No. 2.31e+01; 0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preliminary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #cross-references MUID:96337999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #cross-references MUID:95172389
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Best Local Similarity 71.4%;
Matches 5; Conservative
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Best Local Similarity 100.0%;
Matches 6; Conservative
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ORGANISM
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##status
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KEYWORDS
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#authors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##residues 1-1021 ##label TOM
##cross-references GB:AE000560; GB:AE000511; NID:g2313554; PID:g2313560;
Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Ketchum, K.A.; Klenk, H.P.; Gill, S.; Dougherty, B.A.; Nelson, K.; Quackenbush, J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, K.; Fitzegerald, L.M.; Lee, N.; Adams, M.D.; Hickey, E.K.; Berg, D.E.; Gocayne, J.D.; Utterback, T.R.; Peterson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fulli, C.; Bowman, C.; Watthey, L.; Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.M.; Venter, J.
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RNA-directed DNA polymerase (EC 2.7.7.49), msDNA specific
Escherichia coli retron Ec79
DNA nucleotidyltransferase (RNA-directed); reverse
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#formal_name Escherichia coli retron Ec79
17-Apr.1993 #sequence_revision 15-Oct-1996 #text_change
05-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGR:HP0453
#length 1021 #molecular-weight 120112 #checksum 8085
                                                                                                                                                                                                                                                                 #journal Nature (1997) 388:539-547
#title The complete genome sequence of the gastric pathogen
#cross-references MUD:97394467
#accession E64576
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#title Structure and biosynthesis of unbranched multicopy
single-stranded DNA by reverse transcriptase in a
Escherichia coli isolate.
#cross-references MUID:93116591
                                                                                                                                                                                                                                                                                                                                                                                                       preliminary; nucleic acid sequence not shown; translation not shown
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#length 312 #molecular-weight 35734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 42; DB 2; Le
Pred. No. 1.36e+01;
2; Mismatches 0
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Best Local Similarity 100.0%;
Matches 6; Conservative
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Best Local Similarity 71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##molecule_type DNA
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TITLE

Matches

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SUMMARY

#authors ACCESSIONS

REFERENCE

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Indels

#type complete

D64303

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RESULT

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KEYWORDS SUMMARY

GENETICS

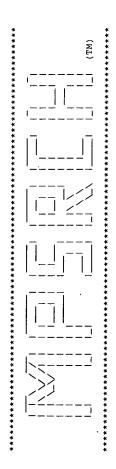
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1 ENKISYO 7
                                                                           667 QDKITYQ
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Biochemistry (1992) 31:12536-12542
Purification and characterization of a carbonic anhydrase II
inhibitor from porcine plasma.
                                                                                                                   S75388 #type complete
probable phenylalanine--tRNA ligase (EC 6.1.1.20) beta chain
- Sulfolbous solfataricus
phenylalanyl-tRNA synthetase beta chain; protein c04021
#formal_name Sulfolobus solfataricus
09-oct-1997 #sequence_revision 24-Oct-1997 #text_change
                                                                                                                                                                                                                                                                                                                                                                          Mol. Microbiol. (1996) 22:175-191
Organizational characteristics and information content of an
archaeal genome: 156 kb of sequence from Sulfolobus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aminoacyl-tRNA synthetase; ATP; ligase; protein biosynthesis #length 544 #molecular-weight 61815 #checksum 7376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##molecule_type DNA
##residues 1-544 ##label SEN
##cross-references EMBL:V08257; NID:g1707772; PID:e283832; PID:g1707793
##experimental_source strain_P2
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#formal_name Sus scrofa domestica #common_name domestic pig
21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change
                                                                                                                                                                                                                                                                                                 Sensen, C.W.; Klenk, H.P.; Singh, R.K.; Allard, G.; Chan, C.C.Y.; Liu, Q.Y.; Penny, S.L.; Young, F.; Schenk, M.E.; Gaasterland, T.; Doolittle, W.F.; Ragan, M.A.; Charlebois,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the nucleotide sequence was submitted to the EMBL Data
Library, September 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid sequence not shown; translation not shown
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#molecular-weight 77634 #checksum 8035
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                                                                                                                                                                                                                                                                                                                                                                                                                                     solfataricus P2.
#cross-references MUD:97055432
#accession 875388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             larity 57.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-Jan-1999
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S73076
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270 ENKLTYQ 276
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1 ENKISYQ 7
                       |||::||
1 ENKISYQ 7
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#title
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Aunol, G.; Agesawara, N.; Moszer, I.; Albertini, A.M.;
Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.;
Bolotina, A.; Borchert, S.; Boriss, R.; Boursier, L.; Brans, A.; Braun, M.; Brighell, S.C.; Bron, S.; Boruillet, S.;
Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
Choi, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.;
Daniel, R.A.; Denizot, F.; Devine, K.M.; Duesterhoeft, A.;
Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.;
Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.;
Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.;
Ehrita, Y.; Furan, S.; Galizzi, A.; Galleron, N.; Ghim, S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandi, G.
Guiseppt, G.; Guy, B.J.; Haga, K.; Harch, C.; Fulta,
C.; R.; Henaua, Y.; Elaerr-Blanchard, M.; Hacah, C.; Robayashi,
Y.; Koetter, P.; Koningstein, G.; Krogh, S.; Komano, M.;
Kurita, K.; Lapidus, A.; Lardinois, S.; Konano, M.;
Kurita, K.; Lapidus, A.; Lardinois, S.; Kobayashi,
Y.; Moestl, D.; Medigue, C.; Medina, N.; Mellado, R.P.; Mizuno,
M.; Moestl, D.; Nakai, S.; Noback, M.; Noone, D.; O'Reilly,
M.; Ogwaw, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro,
V.; Pohl, T.M.; Percecan, E.; Puljic, P.; Purnelle, B.; Rapoport, G.
Rey, M.; Reynolds, S.; Rleger, M.; Ruit, S.; Heyer, E.;
Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scallon, J.;
Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.;
Takemaru, K.; Takeuchi, M.; Tamakoshi, A.; Tanaka, T.;
Terpstra, P.; Yoshide, K.; Vassarotti, A.; Tanaka, T.;
Terpstra, P.; Vassarotti, A.; Vasiai, A.;
Wambutt, R.; Wedler, E.; Wedler, H.; Waitzenegger, T.;
Windenbol, M.; Vashida, K.; Vasharain, R.; Yashida, R.; Yashida, R.; Yoshida, R.; Yoshida, R.; Yoshida, R.; Yoshikawa, H.F.; Zumeto, R.; Yashin, R.; Yashida, R.; Yoshikawa, H.F.; Zumeto, R.; Yashida, R.; Yashida, R.; Yoshikawa, H.F.; Zumeto, R.; Yashida, R.; Yashida, R.; Yoshikawa, H.F.; Zumeto, R.; Yashida, R.; 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##residues 1-176 ##label GLA ##cross references EMBL:X73124; NID:4413923; PID:9580872 ##cross references EMBL:X73124; NID:9413923; PID:9580872 ##note the nucleotide sequence was submitted to the EMBL Data #fnote Library. June 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                   S39702 #type complete transcription antiterminator of sacA/sacP sacT - Bacillus
                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #formal_name Bacillus subtilis
07-0ct-1994 #sequence_revision 22-Nov-1996 #text_change
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Score 41; DB 2; Length 704
Pred. No. 2.31e+01;
3; Mismatches 0; Indels
    85.4%;
larity 57.1%;
Conservative
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##residues 1-2
         Query Match
Best Local Similarity
Matches 4; Conserv
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##cross-references EMBL:D90911; GB:AB001339; NID:g1653083; PID:d1018753; PID:g1653104
##note the nucleotide sequence was submitted to the EMBL Data Library, June 1996.

##note the first 
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hypothetical protein slr1512 - Synechocystis sp. (strain PCC 6803)
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                                                                                                 ##status preliminary; nucleic acid sequence not shown; translation not shown ##molecule_type DNA #residues 1-276 ##label KUN ##cross-references GB:299123; GB:AL009126; NID:g2636240; PID:e1186306; ##experimental_source strain 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *superfamily Bacillus subtilis transcription antiterminator
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#length 276 #molecular-weight 32074 #checksum 7428
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Pred. No. 3.90e+01;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40; DB 2; Length 276;
Pred. No. 3.90e+01;
0; Mismatches 1; Indels
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PCC 6803
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#cross-references MUID:98044033
#accession C69703
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##residues_1-27, "."
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Best Local Similarity 85.7%;
Matches 6; Conservative
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Best Local Similarity 71.4%;
Matches 5; Conservative
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1 ENKISYQ 7
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CLASSIFICATION
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REFERENCE
#authors
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Oct 28 11:34:43 1999; MasPar time 2.06 Seconds 95.967 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-081-707-12 (1-7) from US09081707.pep 48 Description: Perfect Score:

1 ENKISYQ 7 Sequence:

PAM 150 Gap 15 Scoring table:

77977 seqs, 28268293 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

1:swissprot swiss-prot37 Database:

scale 1.126 Mean 21.081; Variance 18.718; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		d¥					
Result No.	Score	Query Match	Query Match Length	DB	QI ,	Description	Prėd. No.
н	48	100.0	582	-	SEM2_HUMAN	SEMENOGELIN II PRECURS	9.82e-02
7	48	100.0	206	Н	SEM2_MACMU	II	9.82e-02
m	43	89.6	709	٦	TOP1_MYCGE	DNA TOPOISOMERASE I (E	2.43e+00
4	42	87.5	384	٦	XYLR_BACSU	SE REPRESSOR.	4.47e+00
5	42	87.5	462	Н	SEM1_HUMAN	SEMENOGELIN I PROTEIN	4.47e+00
9	42	87.5	553	Н	VH65_NPVAC	EARLY 65 KD PROTEIN.	4.47e+00
7	41	85.4	319	٦	Y028_METJA	HYPOTHETICAL PROTEIN M	8.13e+00
80	41	85.4	439	Н	ENO1_SCHPO	ENOLASE (EC 4.2.1.11)	8.13e+00
σ	40	83.3	276	-	SACT_BACSU	SACPA OPERON ANTITERMI	1.46e+01
10	40	83.3	1108	-	CYGF_HUMAN	RETINAL GUANYLYL CYCLA	1.46e+01
11	39	81.3	187	ч	RS4_METJA	30S RIBOSOMAL PROTEIN	2.59e+01
12	39	81.3	381	7	CYB_NOTPE	CYTOCHROME B.	2.59e+01
13	39	81.3		-	PYRP_BACSU	URACIL PERMEASE (URACI	2.59e+01
14	39	81.3	458	٦	YGEH_ECOLI	HYPOTHETICAL 52.8 KD P	2.59e+01
15	39	81.3		-	THI3_YEAST	THIAMINE METABOLISM RE	2.59e+01
16	39	81.3		Н	BAR3_SCHCO	PHEROMONE B ALPHA 3 RE	2.59e+01
17	39	81.3	639	Н	BAR1_SCHCO	PHEROMONE B ALPHA 1 RE	2.59e+01
18	39	81.3	689	Н	YE30_HELPY	HYPOTHETICAL PROTEIN H	2.59e+01
19	39	81.3	1087	Н	PGDS_XENLA	ALPHA PLATELET-DERIVED	2.59e+01
20	39	81.3	1089	Н	NMD2_YEAST	NONSENSE-MEDIATED MRNA	2.59e+01
21	39	81.3	1820	Н	CINA_ELEEL	SODIUM CHANNEL PROTEIN	2.59e+01
22	38	79.2	94	Н	YOGV_BACSU	HYPOTHETICAL 10.5 KD P	4.53e+01
23	38	79.2	145	Н	Y127_MYCGE	HYPOTHETICAL PROTEIN M	4.53e+01

4.53e+01	4.53e+01	4.53e+01	4.53e+01	4.53e+01	4.53e+01	4.53e+01	4.53e+01	4.53e+01	4.53e+01	4.53e+01	4.53e+01	4.53e+01	4.53e+01	4.53e+01	4.53e+01	4.53e+01	7.83e+01	7.83e+01	7.83e+01	7.83e+01	7.83e+01
PROBABLE THIOL PEROXID	GTP-BINDING PROTEIN CI	HYPOTHETICAL 40.9 KD P	ENOLASE (EC 4.2.1.11)	ADENOSYLMETHIONINE-8-A	ACETYLCHOLINE RECEPTOR	REGULATOR OF G-PROTEIN	CTP SYNTHASE (EC 6:3.4	REGULATOR OF G-PROTEIN	VIRION GENE 34 PROTEIN	REPLICATION PROTEIN E1	REPLICATION PROTEIN E1	GLUCOSE INHIBITED DIVI	REPLICATION PROTEIN E1	CHROMOSOMAL REPLICATIO	FLIGHTLESS-I PROTEIN H	HYPOTHETICAL 208 KD PR	HYPOTHETICAL PROTEIN M	HYPOTHETICAL 40.8 KD P	WALL-ASSOCIATED PROTEI	HYPOTHETICAL 83.0 KD P	MAJOR 114 KD STRUCTURA
TPX_STRPA	CIN4_YEAST	YA4F_SCHPO	ENO_TREPA	BIOA_BACSH	ACH6_CAEEL	RGSE_RAT	PYRG_HAEIN	RGSE_MOUSE	UL25_VZVD	VE1_BPV2	VE1_BPV1	GIDA_MYCPN	VE1_PAPVD	DNAA_STRCO	FLIH_CAEEL	YCF1_EPIVI	Y948_METJA	YEV7_YEAST	WAPA_STRMU	YBJ7_YEAST	VP3_RDV
1	-	Н		~1	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	H	Н	Н	-	Н	Н
163	191	349	432	455	487	544	545	547	579	604	605	612	613	959	1257	1738	191	357	445	728	1019
79.2	79.2	79.2	79.2	79.2	79.2	79.2	79.2	79.2	79.2	79.2	79.2	79.2	79.2	79.2	79.2	79.2	77.1	77.1	77.1	77.1	77.1
38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	37	37	37	37	37
24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

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entities requires a license agreement (See http://www.isb-sib.ch/announce/
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EUR. J. BIOCHEM. 245:25-31(1997).
-!- FUNCTION: PARTICIPATE IN THE FORMATION OF A GEL MATRIX ENTRAPPING
THE ACCESSORY GLAND SECRETIONS AND EJACULATED SPERMATOZOA.
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE; 97274635.
ULVSBACK M., LUNDWALL A.;
"Cloning of the semenogelin II gene of the rhesus monkey.
Duplications of 360 bp extend the coding region in man, rhesus monkey and baboon.";
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                       MACACA MULATTA (RHESUS MACAQUE).
EUKARYOTA, METAZOA, CHORDATA, VERTEBRATA, MAMMALIA, EUTHERIA,
PRIMATES, CATARRHINI, CERCOPITHECIDAE, CERCOPITHECINAE, MACACA.
                                                                                                                                    2-1.
2-2.
4 x 60 AA TANDEM REPEATS, TYPE I.
3-2.
                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                            Length 582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 48; DB 1; Length 706;
Pred. No. 9.82e-02;
0; Mismatches 0; Indels
                                                                                                                                                                                                         Score 48; DB 1; Length 582;
Pred. No. 9.82e-02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEMEN; SEMINAL VESICLE; REPEAT; SIGNAL; GLYCOPROTEIN.
                                                                                 SEMEN; SEMINAL VESICLE; REPEAT; SIGNAL; GLYCOPROTEIN.
                                                                                                     SEMENOGELIN II.
REPEAT-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9D5897A8 CRC32;
                                                                                                                                                                            272 PROBABLE.
65445 MW; DD20304E CRC32;
                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-UD-1998 (REL. 36, LAST ANNOTATION UPDATE)
SEMENOGELIN II PRECURSOR (SGII).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
SEMENOGELIN II
         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     706
; 79875 MW;
                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Conservative
                            EMBL; M81651; G307418; -. EMBL; M81652; G338239; -. EMBL; Z47556; E82662; -.
                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X92589; E208370; -.
                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                               559
200
200
500
559
                                                             PIR; A43412; A43412.
MIM; 182141; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                706 AA;
                                                                                                                                                                                       582 AA;
                                                                                                                                                                                                                                                    343 ENKISYQ 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            347 ENKISYQ 353
                                                                                                                                                                                                                                                                 1 ENKISYQ 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ENKISYO 7
                                                                                                                                                                                                                                                                                                                 SEM2_MACMU
Q95196;
                                                                                                                                                                   REPEAT
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                       SEQUENCE
                                                                                                               DOMAIN
REPEAT
                                                                                          SIGNAL
                                                                                                                                    REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IGNAL
                                                                                                                                                         DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA, FOLLOWED BY PASSAGE AND REJOINING.

-! SUBUNT: MONOMER (BY SIMILARITY).

-! WHEN A TOPOISOMERASE TRANSIENITY BREAKS A DNA BACKBONE BOND, IT

SIMULTANEOUSLY FORMS A PROTEIN-DNA LINK, IN WHICH A TYROSYL OXYGEN
IN THE ENZYMS IS JOINED TO A DNA PHOSPHORUS AT ONE END OF THE

ENZYMS—SEVERED DNA SYRAND.

-! SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAINS-ATCC 33530 / G-37;
STRAINS-ATCC 33530 / G-37;
MEDLINE; 96026346.
FRASER C.M., GOCAYNE J.D., WHITE O., ADAMS M.D., CLAYTON R.A.,
FLEISCHMANN R.D., BULT C.J., KERLAVAGE A.R., SUTTON G., RELLEY J.M.,
FLEISCHMANN J.L., WEIDMAN J.F., SMALL K.V., SANDUSKY M., FUHRMANN J.L.,
NGUYEN D.T., UTTERBACK T.R., SAUDEK D.M., PHILLIPS C.A., MERRICK J.M.,
TOMB J.-F., DOUGHERTY B.A., BOTT K.F., HU P.-C., LUCIER T.S.,
FLEISCHMANN SMITH H.O., HUTCHISON C.A. III, VENTER J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. BACTERIOL. 175:7918-7930(1993).
-!- FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES LEADS TO THE CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER.
-!- CATALYZIC ACTIVITY: ATP-INDEPENDENT BREAKAGE OF SINGLE-STRANDED
                                                                                 01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DNA TOPOISOMERASE I (EC. 5.99.1.2) (OMEGA-PROTEIN) (RELAXING ENZYME)
(UNIWISTING ENZYME) (SMIVELASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 399-481 AND 527-657 FROM N.A.
STRAIN=ARCC 33530 / G-37;
MEDLINE; 94075230.

MEDLINE; 94075230.

"A survey of the Mycoplasma genitalium genome by using random
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                               BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; MOLLICUTES;
MYCOPLASMATACEAE; MYCOPLASMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The minimal gene complement of Mycoplasma genitalium."; SCIENCE 270:397-403(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 43; DB 1; L
Pred. No. 2.43e+00;
2; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA CLEAVAGE (BY
18063FDC CRC32;
                               709 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS00396; TOPOISOMERASE_I_PROK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISOMERASE; TOPOISOMERASE; DNA-BINDING.
                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     334 334 D
709 AA; 82544 MW;
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HSSP; P06612; 1ECL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89.6%;
larity 71.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U39691; G1045802; -.
EMBL; U02134; G409912; -.
EMBL; U02242; G407259; -.
                               STANDARD;
                                                                                                                                                                                                                                          TOPA OR MG122.
MYCOPLASMA GENITALIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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| ENKISYQ 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGR; MG122;
PROSITE; PS0(
                                                                                       01-FEB-1996
LT 3
TOP1_MYCGE
P47368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequencing.
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SEQUENCE
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MEDLINE;
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PEPTIDE
                                                                                      seminal
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VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
    EEZZE&X&EEZX&XEEZXXXEEZEEEEEEEEEEEE
                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                 between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 92388176.
ULVSBAECK M., LAZURE C., LILJA H., SPURR N.K., RAO V.V., LOEFFLER C.,
HANSMANN I., LUNDWALL A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LILDA H., ABRAHAMSSON P.-A., LUNDWALL A.;
"Semenogelin, the predominant protein in human semen. Primary
structure and identification of closely related proteins in the male
accessory sex glands and on the spermatozoa.";
J. BIOL. CHEM. 264:1894-1900(1989).
                                                                                                                                                                                                                                                                                                                                                      PRODIE; COLLEY, COLLEY, COLLEY, COLLEY, COLLEY, PEOCH BOLLEY, COLLEY, I TRANSCRIPTION REGULATION; DNA-BINDING; REPRESSOR; XYLOSE METABOLISM. DNA.BIND 29 48 H-T-H MOTIF (BY SIMILARITY).
                                                                                                                                                                                  xylk gene and xyl operator.";
J. BACTERIOL. 171:3840-3845(1989).
-!- FUNCTION: TRANSCRIPTIONAL REPRESSOR OF XYLOSE-UTILIZING ENZYMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                  MEDLINE; 89291732.
KREUZER P., GAERTNER D., ALLMANSBERGER R., HILLEN W.;
"Identification and sequence analysis of the Bacillus subtilis W23
                                                                                              BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE; BACILLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEMENOGELIN I PROTEIN PRECURSOR (SGI) [CONTAINS: SEMINAL BASIC PROTEIN; ALPHA-INHIBIN-92; ALPHA-INHIBIN-31].
                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 42; DB 1; Length 384;
Pred. No. 4.47e+00;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   Length 384;
                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO THE ROK (NAGC/XYLR) FAMILY.
                               CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (REL. 13, LAST SEQUENCE UPDATE)
(REL. 37, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             462 AA.
             384 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                87.5%;
larity 71.4%;
Conservative
                                                                                                                                                                                                                                                                                                                            EMBL; M27248; G143841; -. PIR; A32885, A32885 PROSITE; PS01125; ROK; 1.
             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                          (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-MAR-1987 (REL.
01-JAN-1990 (REL.
15-DEC-1998 (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE; 89109215.
                                 (REL.
                                                                                     BACILLUS SUBTILIS
                                                                XYLOSE REPRESSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                            275 EKKVSYQ 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ENKISYO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEMG1 OR SEMG
                                          01-AUG-1990
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IISSUE-BLOOD
                                01-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
ID SEM1_HUMAN
AC P04279;
           XYLR_BACSU
                                                                                                                                         STRAIN-W23
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STUCTURE.";
PROC. NATL. ACAD. SCI. U.S.A. 82:4041-4044(1985).
PROC. NATL. ACAD. SCI. U.S.A. 82:4041-4044(1985).
-!- FUNCTION: SEMENOGELIN I IS THE PREDOMINANT PROTEIN IN HUMAN SEMEN.
IT PARTICLPATES IN THE PORMATION OF A GEL MATRIX ENTRAPPING THE ACCESSORY GLAND SECRETIONS AND EJACULATED SPERMATOZOA. FRAGMENTS OF SEMENOGELIN AND/OR FRAGMENTS OF SEMENOGELIN AND/OR FRAGMENTS OF SEMENOGELIN AND/OR FRAGMENTED BY THE KALLIKREIN-LIKE THE GEL-FORMING PROTEINS ARE FRAGMENTED BY THE KALLIKREIN-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: ALPHA-INHIBIN-92 AND ALPHA-INHIBIN-31, DERIVED FROM THE PROTECLYTIC DEGRADATION OF SEMENOGELIN, INHIBIT THE SECRETION OF PITUITARY FOLLICLE-STIMMLATING HORMONE.
SUBUNIT: OCCURS IN DISULFIDE-LINKED COMPLEXES WHICH MAY ALSO CONTAIN TWO LESS ABUNDANT 71- AND 76-KD SEMENOGELIN-RELATED
"Gene structure of semenogelin I and II. The predominant proteins in numan semen are encoded by two homologous genes on chromosome 20."; J. BIOL. CHEM. 267:18080-18084(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 AA REPEAT 1.

42 AA REPEAT 2.

58 AA REPEAT 1.

58 AA REPEAT 2.

42 AA REPEAT 3.

42 AA REPEAT 3.

5 -> T (LESS COMMON GENETIC VARIANT).

K -> N (IN REF 2).

697515C7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                       SEIDAH N.G., RAMASHARMA K., SAIRAM M.R., CHRETIEN M.; "Partial amino acid sequence of a human seminal plasma peptide with inhibin-like activity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PYRROLIDONE CARBOXYLIC ACID (PROBABLE)
ALPHA-INHIBIN-91.
SEMINAL BASIC PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Human seminal alpha inhibins: isolation, characterization, and
                                                                                                                                                                  LILJA H., JEPPSSON J.-O.; Amino acid sequence of the predominant basic protein in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT; SIGNAL; POLYMORPHISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 68-159.
MEDLINE; 85216629.
LI C.H., HAMMONDS R.G., RAMASHARMA K., CHUNG D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 42; DB 1; Le
Pred. No. 4.47e+00;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLYPEPTIDES.
TISSUE SPECIFICITY: SEMINAL VESICLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERCHAIN
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                                                                                                                                                                                                                                                          FEBS LETT. 182:181-184(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                  inhibin-like activity.";
FEBS LETT. 167:98-102(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 87.5%;
Best Local Similarity 100.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; J04440; G338019; -.
EMBL; Z47556; E133812; -.
EMBL; M81650; G487420; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEMEN; SEMINAL VESICLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24
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                                                                                                                SEQUENCE OF 108-159.
                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 108-138.
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PIR; A31489; A31489.
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462 AA;
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                                                                                                                                                                                                                                   plasma
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Gaps

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174 ENKISY 179
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                                                                                                                                                                                              TIGR; MJ0028;
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ENO1_SCHPO
P40370;
                                                                          jannaschii.
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Matches
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                                                                                                                                                                                                                                                                     AYRES M.D., HOWARD S.C., KUZIO J., LOPEZ-FERBER M., POSSEE R.D.; "The complete DNA sequence of Autographa californica nuclear polyhedrosis virus."; VIROLOGY 202:586-60(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                            AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).
VIRUSES; DSDNA VIRUSES, NO RNA STAGE; BACULOVIRIDAE;
NUCLEOPOLYHEDROVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-JADA 2661 / ATCC 43067;
MEDIJNE: 96337999.
BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,
                                                                                                                                                                                              BECKER D., KNEBEL-MOEKSDORF D.;
Sequence and temporal appearance of the early transcribed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARCHAEA; EURYARCHAEOTA; METHANOCOCCALES; METHANOCOCCACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 42; DB 1; Length 553; Pred. No. 4.47e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                553 AA; 65576 MW; 420D4413 CRC32;
                                                                                        LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAST SEÓUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                CREATED)
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01-NOV-1997 (REL. 35, LAST SEQ
                                                                                                                                                                                                               baculovirus gene HE65.";
J. VIROL. 67:5867-5872(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL PROTEIN MJ0028.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.5%;
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X73577; G313680; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               METHANOCOCCUS JANNASCHII.
                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                               01-FEB-1995 (REL. 31,
01-FEB-1995 (REL. 31,
01-NOV-1995 (REL. 32,
EARLY 65 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                              MEDLINE; 94303173.
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                                                                                                                                                                           STRAIN=E;
MEDLINE; 93381786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       271 ENKIVYQ 277
       284 NKISYQ 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ENKISYO 7
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                        2 NKISYQ 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997
                                                                                                                                                                                                              baculovirus
                                                              VH65_NPVAC
Q08539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Y028_METJA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCAYNE J.D., KERLAYAGE A.R., DOUGHERTY B.A., TOMB J.-F., ADAMS M.D., REICH G.I., OVERBEER R., KIRKNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODEK A., SCOTT J.L., GEOGRAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D., UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C., COTTON M.D., ROBERTS K.M., HURTH H.O., WOESE C.R., VENTER J.C., "COMPLETE genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE; 95172389.
JACKSON J.C., LOPES J.M.;
A CDNA from Schizzosaccharomyces pombe encoding a putative enolase.";
GENE 154:109-113(1995).
-!- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERAIE = PHOSPHOENOLPYRUVATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  + H(2)O.
-!- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
115-UDL-1998 (REL. 31, LAST ANNOTATION UPDATE)
ENOLASE (EC 4. 2.1.31, (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 8.13e+00;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -:- PATHWAY: GLYCOLXSIS.
-:- SUBUNIT: HOMODIAMER (BY SIMILARITY).
-:- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
-:- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES;
SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL PROTEIN.
SEQUENCE 319 AA; 36160 MW; 606CC6D4 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         439 AA
                                                                                                                                                                                                                                                                                                                                                                                SCIENCE 273:1058-1073(1996).
-!- SIMILARITY: WEAK, TO THE HYPE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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PROSITE; PS00164; ENOLASE; 1.
PFAM; PF00113; enolase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 85.4%;
Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U67461; G1590830; -.
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VISION.
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RA HULLO M.F., IONESCU M., LUBOCHINSKY B., MARCELINO L., MOSZER I.,
A PRESECAN E., SANTARA M., SCHNEIDER E., SCHWEIZER J., VERTES A.,
A PRESECAN E., SANTARA M., SCHNEIDER E., SCHWEIZER J., VERTES A.,
A RAPOPORT G., DANCHIN A.,
A RAPOPORT G.,
A RAPOPO
                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBTILIST; BG10593; SACT.
PROSITE: PS00664; ANTITERMINATORS_BGLG; 1.
PROSITE: PS00674; B91G_antitermin; 2.
HSSP; P15401; 1AUU.
TRANSCRIPTION REGULATION; ACTIVATOR; RNA_BINDING; PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEBARBOUILLE M., ARNAUD M., FOUET A., KLIER A., RAPOPORT G.; "The sacT gene regulating the sacPA operon in Bacillus subtilis shares strong homology with transcriptional antiterminators."; J. BACTERIOL. 172:3966-3973(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
                                                                                                                                                                                                                                 ;
                                                                                                                                                                                      DB 1; Length 439;
                                                                                                                                                                                                                               0; Indels
                                                                   MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
61A96F15 CRC32;
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4FFB1288 CRC32;
                                                                                                                                                                                                         No. 8.13e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                    Score 41; DB 1;
Pred. No. 8.13e+
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     276 AA.
                                                BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; J03006; G143488; ALT_INIT.
EMBL; X73124; G580872; -.
EMBL; Z99123; E1186306; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96
32074 MW;
                                                                                                                                        47323 MW;
                        MAGNESIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1995 (REL. 31, LAST A SACPA OPERON ANTITERMINATOR.
                                                                                                                                                                                    85.4%;
                                                                                                                                                                                                            .arity 71.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                159
246
295
                                           159
246
295
320
439 AA;
                     LYASE; GLYCOLYSIS;
ACT_SITE 159
METAL 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     276 AA;
HSSP; P00924; 1NEL.
                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SACT OR IPA-47D.
BACILLUS SUBTILIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90299824
                                                                                                                                                                                                                                                                            270 ENKLTYQ 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96
                                                                                                                                                                                                                                                                                                         |||::||
ENKISYQ 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1992
01-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                T 9
SACT_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BACILLUS
                                                                                                                                      SEQUENCE
                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT
                                                                                        METAL
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                                                                                                                                                                                                                               Matches
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KW
FT
FT
SO
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Score 40; DB 1; Length 275; Pred. No. 1.46e+01;

83.3%; 85.7%;

Query Match Best Local Similarity

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 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: GTP = 3,'5'-CYCLIC GMP + PYROPHOSPHATE.
ENZYME REGULATION: ACTIVATED BY GCAP-1; INHIBITED BY CALCIUM.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: RETINA. LOCALIZED EXCLUSIVELY IN THE OUTER
NUCLEAR LAYER AND INNER SEGMENTS OF THE ROD AND CONE PHOTORECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTM: THERE ARE 9 CONSERVED CYSTEINE RESIDUES IN SENSORY GUANYLATE CYCLARES, 6 IN THE EXTRACELULAR DOMAIN, WHICH MAY BE INVOLVED IN INTRA- OR INTERCHAIN DISJUEIDE BONDS. SIMILARITY: TO OTHER GUANYLATE CYCLASES. BELONGS TO THE SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THE RODS
NVOLVED IN
                                                                                                                                                      01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
RETINAL GUANYLYL CYCLASE 2 PRECURSOR (EC 4.6.1.2) (GUANYLATE CYCLASE 2F, RETINAL) (REGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLATE CYCLASE 2) (ROS-GC2) (GUANYLATE CYCLASE F) (GC-F).
                                                                                                                                                                                                                                                                                                                                                                                                                                 retina guanylyl cyclase (RetGC), RetGC-2.";
PROC. NATL. ACAD. SCI. U.S.A. 92:5535-5539(1995).
-!- FUNCTION: PROBABLY PLAYS A SPECIFIC FUNCTIONAL ROLE IN THE RODS
AND/OR CONES OF PHOTORECEPTORS. IT MAY BE THE ENZYME INVOLYED IN
THE RESYNTHESIS OF CGMP REQUIRED FOR RECOVERY OF THE DARK STATE
                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 95296345.
LOWE D.G., DIZHOOR A.M., LIU K., GU Q., SPENCER M., LAURA R.,
LU L., HURLEY J.B.;
"Cloning and expression of a second photoreceptor-specific membrane
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGMP SYNTHESIS; SIGNAL; TRANSMEMBRANE; MULTIGENE FAMILY;
 ö
                                                                                                                                                                                                                                                                                      CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RETINAL GUANYLYL CYCLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
 ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN KINASE-LIKE.
                                                                                                                            1108 AA
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM; 300041; --
PROSITE; PS00452; GUANVLATE_CYCLASES; 1.
PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF01094; ANF_receptor; 1.
HSPP; QO2846; 1ANF_LESS; SIGNAL; TRANSMEMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ᆏ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC
                                                                                                                                                                                                                                                                     HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRA
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OF SENSORY GUANYLATE CYCLASES.
 .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AFTER PHOTOTRANSDUCTION.
                                                                                                                                                                                                                                                          GUCY2F OR GUC2F OR REIGC2.
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L37378; G945225; -.
                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50
1108
467
490
1108
810
1064
132
452
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                               194 ENSISYQ 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51
51
52
44
52
452
452
460
                                                             7
                                                                                                                                                                                                                                                                                                                                                   TISSUE=RETINA;
                                                     1 ENKISYQ
 ;
6
                                                                                                             LI 10
CYGF_HUMAN
P51841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
TRANSMEM
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Best Loca Matches

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                                                                                                                                                                                             -:- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
COUPLED TO ATP SYNTHESIS.
-!- CATALYTIC ACTIVITY: OH(2) + 2 FERRICYTOCHROME C = Q +
2 FERROCYTOCHROME C.
-!- COACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
BOUND TO THE PROTEIN.
-!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CYTOCHROME C1 AND THE RIESRE PROTEIN.
                                                          PFAM; PF00033; cytochrome_b_N; 1.
ELECTRON TRANSPORT; MITOCHONDRION; RESPIRATORY CHAIN; TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QUINN C.L., STEPHENSON B.T., SWITZER R.L.; "Functional organization and nuclectide sequence of the Bacillus subtilis pyrimidine blosynthetic operon."; J. BIOL. CHEM. 266:9113-9127(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BACILLUS SUBILLIS.
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
        EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
PALAEOGNATHAE; TINAMIFORMES; TINAMIDAE; NOTHOPROCTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IRON 1 (HEME B562 A.
IRON 2 (HEME B566 A.
IRON 2 (HEME B562 A.
IRON 1 (HEME B566 A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 39; DB 1; Louin Pred. No. 2.59e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71AC7B13 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PYRP_BACSU STANDARD; PRT; 434 AA. P39766; P25982; 01-MAY-1992 (REL. 22, CREATED) 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE) 01-NOY-1995 (REL. 32, LAST ANNOTATION UPDATE) URACIL PERMEASE (URACIL TRANSPORTER).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U76053; G2198708; -.
PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
PROSITE; PS00193; CYTOCHROME_B_QO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 94266724.
TURNER R.J., LU Y., SWITZER R.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM; PF00032; cytochrome_b_C; 1.
PFAM: PF00033; cytochrome_b_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REVISIONS, AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42895 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81.3%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84
98
183
197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      381 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE; 91225016.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       374 ENKILYQ 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BACILLUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HEME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,
SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCANE J.D.,
KERLAVAGE A.R., DOUGHERTY B.A., TOMB J.-F., ADMS M.D., REICH C.I.,
OVERBEEK R., KIRKNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODEK A.,
SCOTT J.L., GEOGHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D.,
UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C.,
COTTON M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BORDOVSKY M.,
KLENK H.-P., FRASER C.M., SMITH H.O., WOBSE C.R., VENTER J.C.,
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1- SIMILARITY: BELONGS TO THE S4P FAMILY OF RIBOSOMAL PROTEINS
                                                                                  .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                        Score 40; DB 1; Length 1108;
Pred. No. 1.46e+01;
                                                                                                                                                                                                                                                                                                                                                                                            ARCHAEA; EURYARCHAEOTA; METHANOCOCCALES; METHANOCOCCACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 39; DB 1; Length 187; Pred. No. 2.59e+01;
                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
    F119341A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187 AA; 22050 MW; CFB127A2 CRC32;
                                                                                                                                                                                                                                                                       01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
10-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
30S RIBOSOMAL PROTEIN 54P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-DEC-1998 (REL. 37, CREATED)
15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
                                                                                Mismatches
                                                                                                                                                                                                                                     187 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       381 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MTCYB OR COB OR CYTB.
NOTHOPROCTA PERDICARIA (CHILEAN TINAMOU).
MITOCHONDRION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE; 96337999.
                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE: PS00632; RIBOSOMAL_S4; 1. PFAM; PF00163; S4; 1. RIBOSOMAL PROTEIN.
1108 AA; 124821 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81.3%;
                                        83.3%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCIENCE 273:1058-1073(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U67475; G1498964; -.
                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                          METHANOCOCCUS JANNASCHII.
                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                          Local Similarity
                                                                                                                  157 DNKISY 162
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                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                              METHANOCOCCUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MJ0190;
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                                                                                                                                          : | | | | |
1 ENKISY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ENKISY
                                                                                                                                                                                                               LT 11
RS4_METJA
P54020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     jannaschii
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CYB_NOTPE
  SEQUENCE
                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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RESULT SERVICE SOLD SERVICE SOL

Matches

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Gaps

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1; Indels

AXIAL LIGAND).
AXIAL LIGAND)
AXIAL LIGAND)

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350 ESKLSYQ 356
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1 ENKISYQ 7
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                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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STRAID*ALZ / MG1655,
MEDLINE: 97426617.
BLATINER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,
RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,
GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
MAU B., SHAO Y.;
"Regulation of the Bacillus subtilis pyrimidine biosynthetic (pyr)
                             J. BACTERIOL. 176:3708-3722(1994).
-!- FUNCTION: TRANSPORT OF URACIL IN THE CELL.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
-!- SIMILARITY: BELONGS TO THE XANTHINE/URACIL PERMEASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
HYPOTHETICAL 52.8 KD PROTEIN IN KDUI-LYSS INTERGENIC REGION.
           gene cluster by an autogenous transcriptional attenuation
                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complete genome sequence of Escherichia coli K-12."; VCE 277:1453-1474(1997).
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F5EFF661 CRC32;
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PFAM; PF00860; Xan_ur_permease; 1.
TRANSPORT; TRANSMEMBRANE.
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llarity 57.1%;
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434 AA;
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                      mechanism.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EURARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
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NISHIMURA H., NOSAKA K., KANEKO Y., WATANABE K., IWASHIMA A.;
SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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-!- FUNCTION: INVOLVED IN THE POSITIVE REGULATION OF THIAMIN
                                                                                                                                                                                                                                                                                    Length 458;
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Pred. No. 2.59e+01;
2; Mismatches 0;
                                                                                                                                                                                                                                                                              Score 39; DB 1; Le
Pred. No. 2.59e+01;
2; Mismatches 0;
                                                                                                                                                                                                                          52752 MW; 4ECE662D CRC32;
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FLAVOPROPEIN; THIAMINE PYROPHOSPHATE.
SEQUENCE 609 AA; 68366 MW; D4C65440 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THIS YEAST STANDARD; PRT; 609 AA. 007471; P89098; 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE) 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE) THIMAINE METABOLISM REGULATORY PROTEIN THIS. THIS OR YDLOBOC.
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larity 71.4%;
Conservative
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ilarity 71.4%;
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                                                                                                             EMBL; U28375; G887803;
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

MasPar time 4.26 Seconds 89.788 Million cell updates/sec Thu Oct 28 11:35:06 1999; Tabular output not generated. Run on:

>US-09-081-707-12 (1-7) from US09081707.pep Description: Perfect Score:

1 ENKISYQ 7 Sequence: PAM 150 Gap 15 Scoring table:

Post-processing: Minimum Match 0% Listing first 45 summaries

179066 segs, 54579741 residues

Searched:

Database:

sptrembl9
1:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human
5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle
9:sp\_phage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified
13:sp\_vertebrate 14:sp\_virus

Mean 20.335; Variance 21.516; scale 0.945 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	Pred. No.	2.29e+00	2.29e+00	4.00e+00	2.04e+01	2.04e+01	2.04e+01	3.44e+01	3.44e + 01	3.44e + 01	3.44e + 01	3.44e + 01	5.75e+01	5.75e+01	5.75e+01	5.75e+01	5.75e+01	5.75e+01	5.75e+01	5.75e+01	5.75e+01
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æ	Query	95.8	95.8	93.8	87.5	87.5	87.5	85.4	85.4	85.4	85.4	85.4	83.3	83.3	83.3	83.3	83.3	83.3	83.3	83.3	83.3
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003635 026425 026425 099003 099003 099003 001207 001325 001525 001525 001525 001525 001525 001525 001525 001525 001525 001525 001525 001525 001525 001525	ALIGNMENT PRT;	CREATI	SIMONS Bentially :	Score Pred. 1; 1		PR' CREAT LAST LAST
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00000000000000000000000000000000000000	20.		RR	Query Best I Matche	Db	RESULT 1D AC OODT DT OODT OODT OODT OOC OC B POOC OC P POOC OC

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NATURE 368:32-38(1994).
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1 ENKISYQ 7
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                       SEOUENCE
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P75377
P75377;
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SEQUENCE FROM N.A.

SEQUENCE PROLINE; 94150718

MEDLINE; 94150718

AND STRAIN-BRIGGOUGH R., ANDERSON K., BAYNES C., BEEKS M.,

MILSON R., AINSCOUGH R., CONNELL M., COPSEY T., COOPER J., COULSON A.,

BONFIELD J., BURTON J., CONNELL M., FAVELLO A., FULTON L.,

A CARATON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

A DONES M., KERSHEN P., HAWKINS T., HILLER L., JIER M., JOHNSTON L.,

A LIGHTNING J., LLOYD C., MOWURRAY A., MORTIMORE B., O'CALLAGHAN M.,

A PARSONS J., PERCY C., RIFKEN L., ROOPRA N., SAUNDERS D., SHOWNKEEN R.,

A MALDON N., SMITH A., SONNIAAMER E., STADEN R., SULSTON J.,

THERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,

A WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

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                                                                                                                                                                                                                                                                                                                     STRAIN-OKLAHOMA;
MEDLINE; 98321180.
REDDY G.R., SULSONA C.R., BARBET A.F., MAHAN S.M., BURRIDGE M.J.,
ALLEMAN, A.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAENORHABDITIS ELEGANS.
EURARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIDA;
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                                                                                                                                                                                                           01-NOV-1998 (TREMBLREL. 08, CREATED)
01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
EHRLICHIA CANIS.
BACTERIA, PROTEOBACTERIA, ALPHA SUBDIVISION, RICKETTSIALES,
RICKETTSIACEAE; EHRLICHIEAE; EHRLICHIA.
                                                                   Length 546;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 45; DB 2; Length 287; Pred. No. 4.00e+00;
                                                                   Score 46; DB 2; Length 546;
Pred. No. 2.29e+00;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
      LORING WELLORS A.;
SUBMITTED (DEC-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U42028; G1353671; -
SEQUENCE 546 AA; 60815 MW; 84B6A9DA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                              of the tribe Ehrlichiae.";
BIOCHEM. BIOPHYS. RES. COMMUN. 247:636-643(1998).
EMBL; AF062762; G3327965; -.
                                                                                                                                                                                                                                                                                                                                                                                                                   287 AA; 32014 MW; 1216502E CRC32;
                                                                                                                                                                                       287 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  875 AA
                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08,
08,
                                                                                                                                                                                                                                                                                                                                                                                                                                          93.8%;
similarity 85.7%;
6; Conservative
                                                                    Ouery Match
Best Local Similarity 85.7%;
                                                                                             Conservative
                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity
Matches 6; Conser
STRAIN-SEROTYPE 1;
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 QNKISYQ 220
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                                                                                                                  57 EDKISYQ 63
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1 ENKISYQ 7
                                                                                                                                         1 ENKISYQ 7
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                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                            RESULT 3
ID 085359
AC 085359;
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076698
076698;
                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).
BACTERIA; PROTEOBACTERIA; EPSILON SUBDIVISION; HELICOBACTER GROUP;
HELICOBACTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIMMELREICH R., HILBERT H., PLAGENS H., PIRKL E., LI B.C.,
                                                                                                                                                                                                                                                                               Score 42; DB 5; Length 875; Pred. No. 2.04e+01; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-M129;
HIMMELREICH K., HILBERT H., LI B.-C.;
BUBLITTED (NOV-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AE000042; G1674117; ...
                      STRAIN-BRISTOL N2;
CLARKE K., ROHLETNG T., MORRIS M.;
"The sequence of C. elegans cosmid T17A3.";
SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                           SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF078787; G3329644; -.
SEQUENCE 875 AA; 99346 MW; 57A375A8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 42; DB 2; L
Pred. No. 2.04e+01;
1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101086 MW; 94D217E0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         879 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1021 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pneumoniae.";
NUCLEIC ACIDS RES. 24:4420-4449(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQ
01-NOV-1998 (TREMBLREL. 08, LAST ANW
HYPOTHETICAL 120.1 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MYCOPLASMATACEAE; MYCOPLASMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02,
                                                                                                                                                                                                                                                                               Query Match 87.5%;
Best Local Similarity 85.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87.5%;
Similarity 71.4%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1997 (TREMBLREL.
01-FEB-1997 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F11_ORF879 PROTEIN.
MYCOPLASMA PNEUMONIAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  879 AA;
                                                                                                                              SEQUENCE FROM N.A. STRAIN-BRISTOL N2; WATERSTON R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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FROM N.A.
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MEDLINE; 97105885
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Gaps

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SEQUENCE

Matches

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LT 7 065412 065412;

RESULT

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STRAIN=IL1403;
MEDLINE; 98101492.
SCHOULER C., CLIER F., LERAYER A.L., EHRLICH S.D., CHOPIN M.C.;
"A type IC restriction-modification system in Lactococcus lactis.";
J. BACTERIOL. 180:407-411(1998).
EMBL; U90222; G2865241; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Structure and biosynthesis of unbranched multicopy single-stranded DNA by reverse transcriptase in a clinical Escherichia coli isolate.";
                                                    PLASMID PIL2614.
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
ESCHERICHIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 41; DB 2; Length 312;
Pred. No. 3.44e+01;
                                                                                                                                                                                                                                                                                                         Length 292;
                                                                                                                                                                                                                                                                                                                                              0; Indels
                (AB1420) GENES, COMPLETE CDS (HSDR) (HSDS) (AB1420).
LACTOCOCCUS LACTIS (STREPTOCOCCUS LACTIS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1997 (TREMBLREL. 03, CREATED)
01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
PHENYLALANYL-TRNA SYNTHETASE ALPHA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                         Score 41; DB 2; Louis Pred. No. 3.44e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOC. MICROBIOL. 6:3531-3542(1992).

EMBL; Z12832; G42501; -.

PFAM; PF00078; rvt; 1.

SEQUENCE 312 AA; 35734 WW; E0E2B0BE CRC32;
                                                                                                                                                                                                                                                                       292 AA; 34223 MW; 9EEÉ797D CRC32;
HSDS), AND PHAGE ABORTIVE INFECTION PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CREATED)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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01,
08,
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Matches 6; Concountry
                                                                                                                                                                                                                                                                                                           85.4%;
71.4%;
                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SULFOLOBUS SOLFATARICUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=CLINICAL STRAIN;
MEDLINE; 93116591.
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                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                         SEQUENCE FROM N.A.
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MEDLINE; 97055432.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESCHERICHIA COLI.
                                                                                                                                                                                                                                                                                                                                                                              23 QNKISYE 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175 ENKISY 180
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1 ENKISYQ 7
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                                                                                       LACTOCOCCUS.
                                                                                                                                                                                                                                                                       SEQUENCE
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P95960
P95960;
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047526
047526;
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EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
           MEDLINE, 97394467.

TOMB J.-F., WHITE O., KERLAVAGE A.R., CLAYTON R.A., SUTTON G.G., FLEISCHMANN R.D., KETCHUM K.A., KLENK H.-P., GILL S., DOUGHERTY B.A., NELSCHMANN K., QUACKERBUSH J., ZHOU L., KIRKNESS E.F., PETERSON S., LOFTUS B., RICHARDSON D., DODSON R., KHALAK H.G., GLODEK A., MCKENNEY K., FITZGERALD L.M., LEE N., ADAMS M.D., HICKEY E.K., BERG D.E., GOCAINE J.D., UTTERBACK T.R., PETERSON J.D., KELLEY J.M., COTTON M.D., WEIDMAN J.M., FUJII C., BOWMAN C., WATTHEY L., WALLIN E., HAYES W.S., BORODOVSKY M., KARP P.D., SMITH H.O., FRASER C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                         "The complete genome sequence of the gastric pathogen Helicobacter pylori[published erratum appears in Nature 1997 Sep 25.389(649):412].";
NATURE 388:539-547(1997).
EMBL: AE000560; G2313560; -.
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BEVAN M., PETERS S.A., VAN STAVEREN M., DIRKSE W., STIEKEMA BANCROFT I., MEWES H.W., MAYER K., SCHUELLER C.; SUBMITTED (APR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                            Length 1021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41; DB 10; Length 282;
Pred. No. 3.44e+01;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                          Score 42; DB 2; Length 1021 Pred. No. 2.04e+01; 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EU ARABIDOPSIS SEQUENCING PROJECT;
SUBMITIED (ARR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL: ALO25603: E1287836;
HYPOTHETICAL PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
HYPOTHETICAL 31.5 KD PROTEIN.
F18E5.90.
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                      1021 AA; 120112 MW; 3002FBB2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31535 MW; E5572824 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           282 AA.
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ID 054429
AC 054429
AC 054429
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUEND)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUEND)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTADE PLASMID PILISEL REPLICATION PROTEIN DE (REDB), TYPE IC RESTRICTION SUBUNIT DE (HSDM), TYPE IC MODIFICATION SUBUNIT DE (HSDM), TYPE IC MODIFICATION SUBUNIT DE (HSDM), TYPE IC MODIFICATION SUBUNIT
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Matches 5: Conscient
                                                                                                                                                                                                                                                                                                                                                                           Similarity 71.4%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                            87.5%;
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                                                                                                                                                                                                                                                                                                     HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             282 AA;
                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                               558 EEKIAYQ 564
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1 ENKISYQ 7
                                                                                                                                                                                                                                                                                      FIGR; HP0453;
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| ENKISYQ
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Gaps

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Indels

SEQUENCE

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[2]
SEQUENCE FROM N.A.
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1 ENKISY
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SEQUENCE
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P73953
                           VIMM)
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PORCINE INHIBITOR OF CARBONIC ANHYDRASE.

2 2E961A99 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                 Gaps
SENSEN C.W., KLENK H.P., SINGH R.K., ALLARD G., CHAN C.C.Y., LIU O. PENNY S.L., YOUNG F., SCHENK M.E., GAASTERLAND T., DOOLITILE W.F., RAGAN M.A., CHARLEBOIS R.L.;
"Organizational characteristics and information content of an archaeal genome: 156 kb of sequence from Sulfolobus solfataricus
                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 97254619.
WHOBBENS M.W., ROUSH E.D., DECASTRO C.M., FIERKE C.A.;
"Cloning, sequencing, and recombinant expression of the porcine inhibitor of carbonic anhydrase: a novel member of the transferrin
                                                                                                                                                                                                                                                                                                         "Purification and characterization of a carbonic anhydrase II inhibitor from porcine plasma."; BIOCHEMISTRY 31:12536-12542(1992).
                                                                                                               .
0
                                                                                                                                                                                                                                            SUS SCROFA (PIG).
EURARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
ARTIODACTYLA; SUIFORMES; SUINA; SUIDAE; SUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 41; DB 6; Length 704; Pred. No. 3.44e+01; 3; Mismatches 0; Indels
                                                                                              Score 41; DB 1; Length 544; Pred. No. 3.44e+01; 3; Mismatches 0; Indels
                                                                                                                                                                                                   01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
PORCINE INHIBITOR OF CARBONIC ANHYDRASE PRECURSOR.
                                                 MOL. MICROBIOL. 22:175-191(1996).

EMBL; Y08257; E283832; -.

AMINOACYL-TRNA SYNTHETASE.

SEQUENCE 544 AA; 61815 MW; 1C2FFA45 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  232 AA.
                                                                                                                                                                                    704 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         061538;
C1-NOV-1996 (TREMBLREL, 01, CREATED)
                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77634 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85.4%;
                                                                                              Match 85.4%;
Local Similarity 57.1%;
nes 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     larity 57.1%;
Conservative
                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
MEDLINE; 93099129.
ROUSH E.D., FIERKE C.A.;
                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 7
704 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 4; Conser
                                                                                                                                                                                                                                                                                                                                   [2]
SEQUENCE FROM N.A.
                                                                                                                                459 DNKVSYE 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                667 QDKITYQ 673
                                                                                                                                           :||:||:
1 ENKISYQ 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENKISYO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                               Query Match
                                                                                                                                                                          LT 11
Q29545
Q29545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LT 12
Q61538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Н
                                                                                                               Matches
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MUS MÚSCULUS (MOUSE).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDAIA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 85033926.
MEDLINE; 85033926.
KNON B. S., WEISSMAN S.M.;
MOUSE mammary tumor virus-related sequences in mouse lymphocytes are inducible by 12-O-tetradecanoyl phorbol-13-acetate.";
J. VIROL. 52:1000-1004(1984).
EMBL; M11024; G193081;
POLYPROTEIN; ENVELOPE PROTEIN.
                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
ENDOGENOUS MAMMARY TUMOR VIRUS (MMTV) RNA, ENV GENE AND RIGHT LTR
                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40; DB 11; Length 362;
Pred. No. 5.75e+01;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                 Length 232;
                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYNECHOCYSTIS SP. (STRAIN PCC 6803).
BACTERIA; CYANOBACTERIA; CHROOCOCCALES; SYNECHOCYSTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TABATA S.;
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P73953;
01-FBB-1997 (TREMBLREL. 02, CREATED)
01-FBB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
HYPOTHETICAL 39.6 KD PROPEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LT 13
061536
061536
061536;
01536;
01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1998 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
ENVELOPE POLYPROPIEN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                 Score 40; DB 11; I
Pred. No. 5.75e+01;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        362 AA; 40429 MW; DD234921 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 374 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     y Match
Local Similarity 83.3%;
hes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 83.3%;
Similarity 83.3%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-PCC6803;
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Search completed: Thu Oct 28 11:35:53 1999 Job time: 47 secs.

STRAIN-PCC6803;

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

X MEDLINE; 94150718.

A WILSON R., BUSTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,

BONFIELD J., BUSTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,

CRAXTON M., DERR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

GARDNER A., GREEN P., HAMKINS T., HILLIER M., JOHNSTON L.,

JONES M., KERSHAW J., LAISTER N., LATREILLE P.,

LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,

RAFSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,

THIERRY-MEGG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,

WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

T. 2.2 ND of contiguous nucleotide sequence from chromosome III of C.
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               MEDLINE; 97061201.
KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
MIYALIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA S.,
SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,
TABATA S.;
                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                             F56All.3.
GARONGHABDITIS ELEGANS.
EUKARYOTA: METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                     Score 40; DB 2; Length 374;
Pred. No. 5.75e+01;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 40; DB 5; Length 462;
Pred. No. 5.75e+01;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
WATERSTON R.;
WAISTRESTON R.;
SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF038619; G2702456; -.
SEQUENCE 462 AA; 52648 MW; 7FB30B7A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A..
STRAIN=BRISTOL N2;
STRAIN=BRISTOL N2;
GATTUNG S., GOEGA, D., HARPER M.;
SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06, CREATED)
06, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                               374 AA; 39647 MW; F80260FC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  462 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83.3%;
Similarity 57.1%;
4; Conservative
                                                                                                                                                                                                                                                                                     83.3%;
                                                                                                                                                                                                                                                                                                       Similarity 71.4%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                044516;
01-JUN-1998 (TREMBLREL.
01-JUN-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NATURE 368:32-38(1994)
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 4; Conser
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1 ENKISYQ 7
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1 ENKISYQ 7
                                                                                                                                                                                                                                                   SEQUENCE
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ID 044516
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